

FIG. 1A

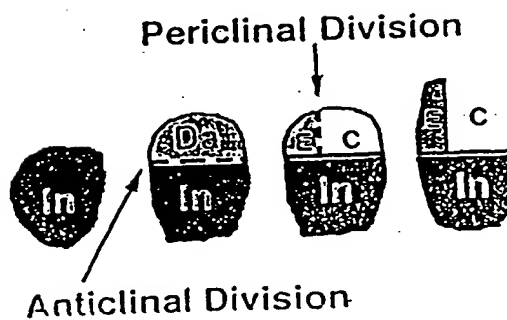


FIG. 1B



FIG. 2A



FIG. 2B

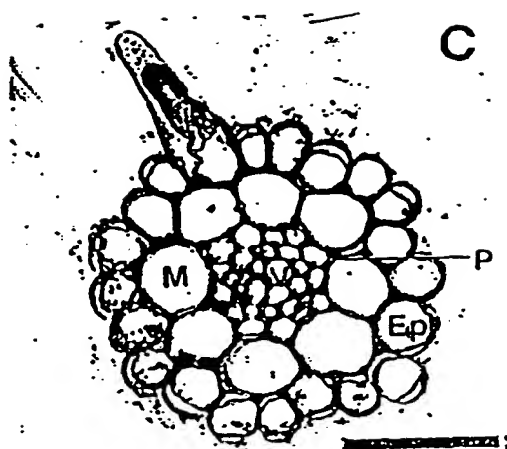


FIG. 2C

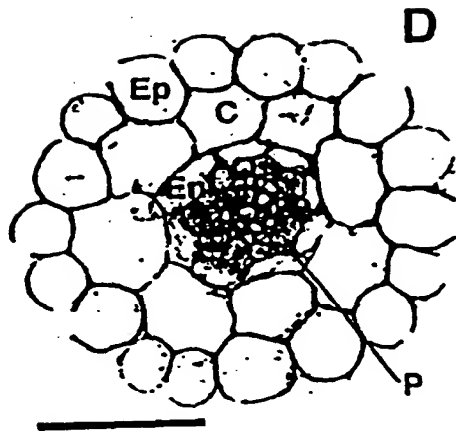


FIG. 2D

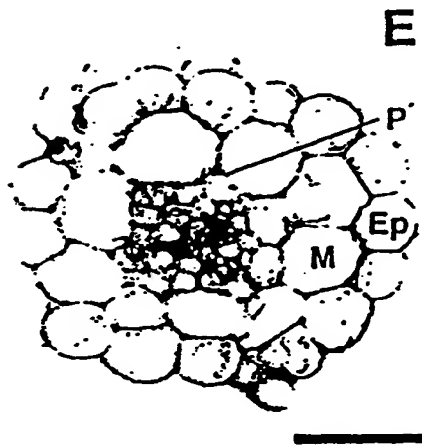


FIG. 2E

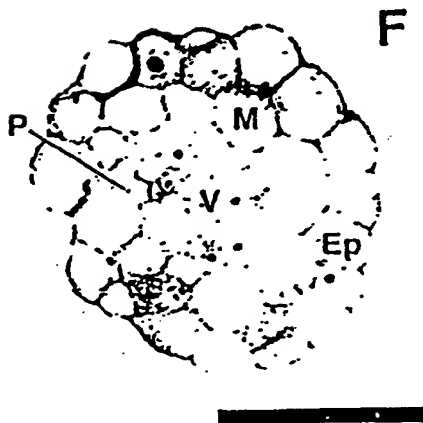


FIG. 2F

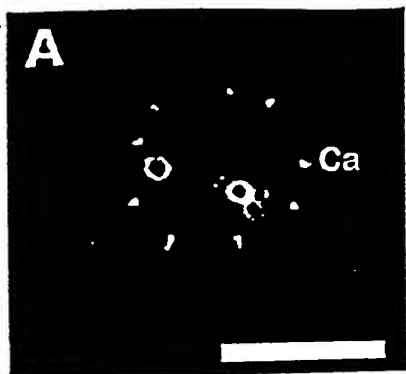


FIG. 3A

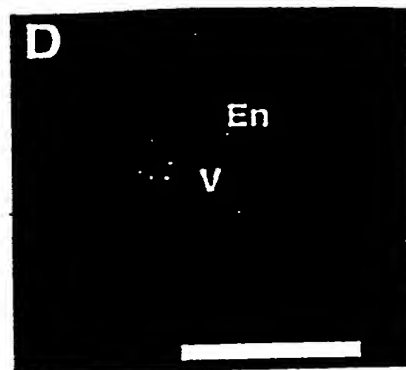


FIG. 3D

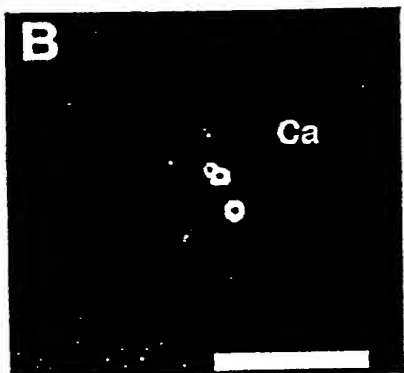


FIG. 3B

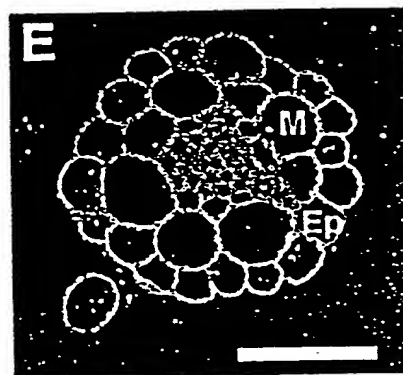


FIG. 3E

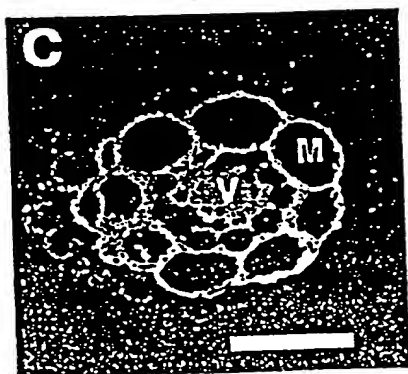


FIG. 3C

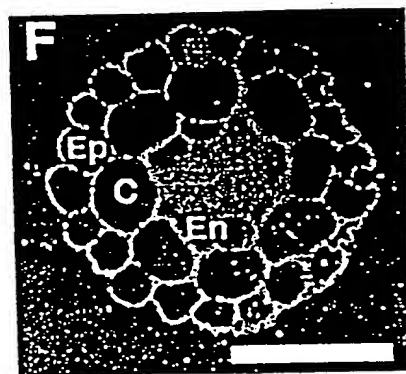


FIG. 3F

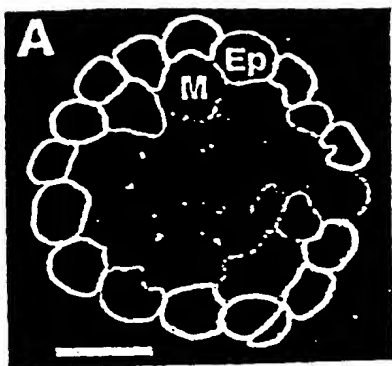


FIG. 4A

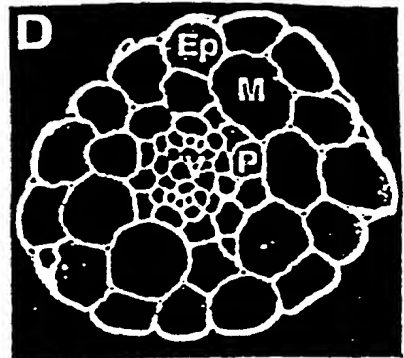


FIG. 4D

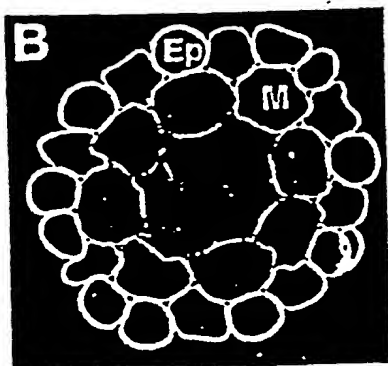


FIG. 4B

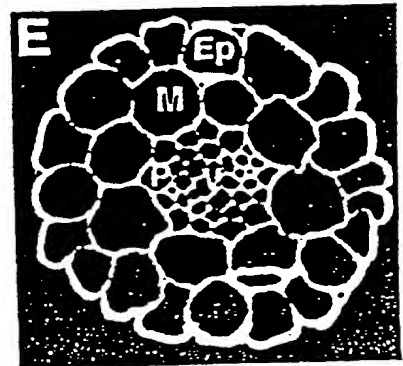


FIG. 4E

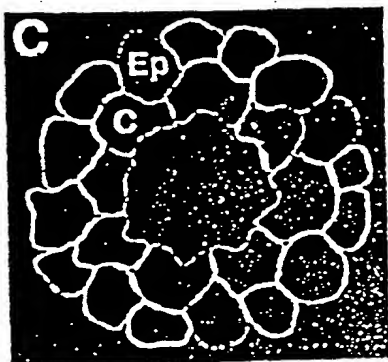


FIG. 4C

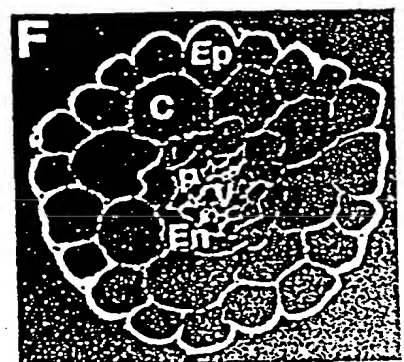
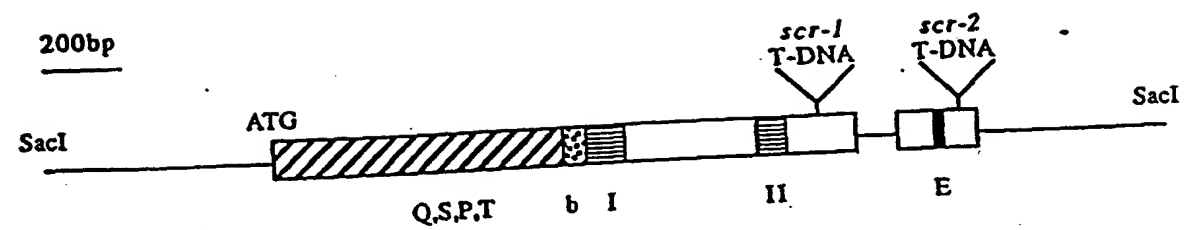


FIG. 4F

09265585-031099

[illegible]

FIG. 5A



probe

a

b

FIG. 5B

660TFO" 58559260

09265585.031099

SCR bZIP-like domain		PAVQTNTAEALRERKEEIKRQKQ	1
		:	D
GCN4	(yeast)	LKRARNTEAARRSRARKLQRMKQ	L
TGA1	(Arabidopsis)	RRLAQNREAARKSRLRKKAYVQQ	L
C-Fos	(mouse)	IRREERNKMAAAKCRNRRRELTD	L
c-JUN	(human)	RKRMRNRIAASKCRKKLERIAR	L
CREB	(human)	VRLMKNREAARECRKKKEYVKC	L
Opaque-2	(maize)	KRKESNRESARRSRYRKAHLKE	L
OBF2	(maize)	MRQIRNRDSAMKSRERKKSYIKD	L
RAF-1	(rice)	RRMVSNNRESARRSRKKKQAHLD	L

FIG. 5C

092655Z 031099
660TED 58559260

SCR.VHIID domain

		1
SCR	AFEKEDSVHIIDL	DIMQGLQWPGLFHILASRPGGPPHVRLTGL
F13896	AVKNESFVHIIDFQISQGGQWVSLIRALGARPGGPPNVRITGI	
Z37192	AMEGEKMHVIDLDASEPAQWLALLQAFNSRPEGPPHLRITGV	
Z25645	AIKGEEVHIIDFDINQGNQYMTLIRIA	
D41474	IHVIDFXLGVGGQWASFLQELAHRRG	
T18310	VHIIXFXLMQGLQWPALMDVFSARKGGPPKLRLITGI	

FIG. 5D

031099 555555

MetAlaGluSerGlyAspPheAsnGlyGlyGlnProProProHisSerProLeuArgThr
ThrSerSerGlySerSerSerSerAsnAsnArgGlyProProProProProProPr Pro
LeuValMetValArgLysArgLeuAlaSerGluMetSerSerAsnProAspTyrAsnAsn
SerSerArgProProArgArgValSerHisLeuLeuAspSerAsnTyrAsnThrValThr
ProGlnGlnProProSerLeuThrAlaAlaAlaThrValSerSerGlnProAsnProPro
LeuSerValCysGlyPheSerGlyLeuProValPheProSerAspArgGlyGlyArgAsn
ValMetMetSerValGlnProMetAspGlnAspSerSerSerSerSerAlaSerProThr
ValTrpValAspAlaIleIleArgAspLeuIleHisSerSerThrSerValSerIlePro
GlnLeuIleGlnAsnValArgAspIleIlePheProCysAsnProAsnLeuGlyAlaLeu
LeuGluTyrArgLeuArgSerLeuMetLeuLeuAspProSerSerSerSerAspProSer
ProGlnThrPheGluProLeuTyrGlnIleSerAsnAsnProSerProProGlnGlnGln
GlnGlnHisGlnGlnGlnGlnGlnGlnHisLysProProProProProIleGlnGlnGln
GluArgGluAsnSerSerThrAspAlaProProGlnProGluThrValThrAlaThrVal
ProAlaValGlnThrAsnThrAlaGluAlaLeuArgGluArgLysGluGluIleLysArg
GlnLysGlnAspGluGluGlyLeuHisLeuLeuThrLeuLeuLeuGlnCysAlaGluAla
ValSerAlaAspAsnLeuGluGluAlaAsnLysLeuLeuLeuGluIleSerGlnLeuSer
ThrProTyrGlyThrSerAlaGlnArgValAlaAlaTyrPheSerGluAlaMetSerAla
ArgLeuLeuAsnSerCysLeuGlyIleTyrAlaAlaLeuProSerArgTrpMetProGln
ThrHisSerLeuLysMetValSerAlaPheGlnValPheAsnGlyIleSerProLeuVal
LysPheSerHisPheThrAlaAsnGlnAlaIleGlnGluAlaPheGluLysGluAspSer
ValHisIleIleAspLeuAspIleMetGlnGlyLeuGlnTrpProGlyLeuPheHisIle
LeuAlaSerArgProGlyGlyProProHisValArgLeuThrGlyLeuGlyThrSerMet
GluAlaLeuGlnAlaThrGlyLysArgLeuSerAspPheThrAspLysLeuGlyLeuPro
PheGluPheCysProLeuAlaGluLysValGlyAsnLeuAspThrGluArgLeuAsnVal
ArgLysArgGluAlaValAlaValHisTrpLeuGlnHisSerLeuTyrAspValThrGly
SerAspAlaHisThrLeuTrpLeuLeuGlnArgLeuAlaProLysValValThrValVal
GluGlnAspLeuSerHisAlaGlySerPheLeuGlyArgPheValGluAlaIleHisTyr
TyrSerAlaLeuPheAspSerLeuGlyAlaSerTyrGlyGluGluSerGluGluArgHis
ValValGluGlnGlnLeuLeuSerLysGluIleArgAsnValLeuAlaValGlyGlyPro
SerArgSerGlyGluValLysPheGluSerTrpArgGluLysMetGlnGlnCysGlyPhe
LysGlyIleSerLeuAlaGlyAsnAlaAlaThrGlnAlaThrLeuLeuLeuGlyMetPhe
ProSerAspGlyTyrThrLeuValAspAspAsnGlyThrLeuLysLeuGlyTrpLysAsp
LeuSerLeuLeuThrAlaSerAlaTrpThrProArgSerSTOP

FIG. 5E

09265585.031099

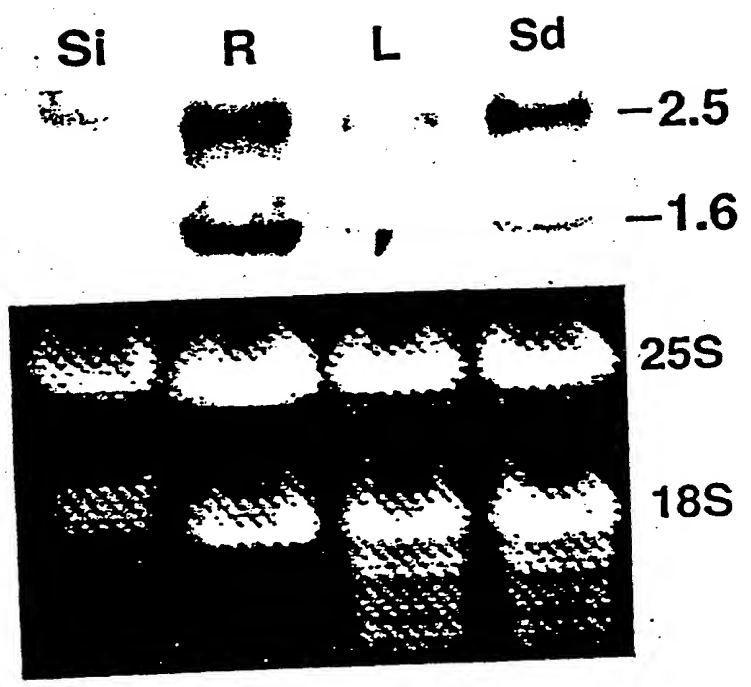


FIG. 6A

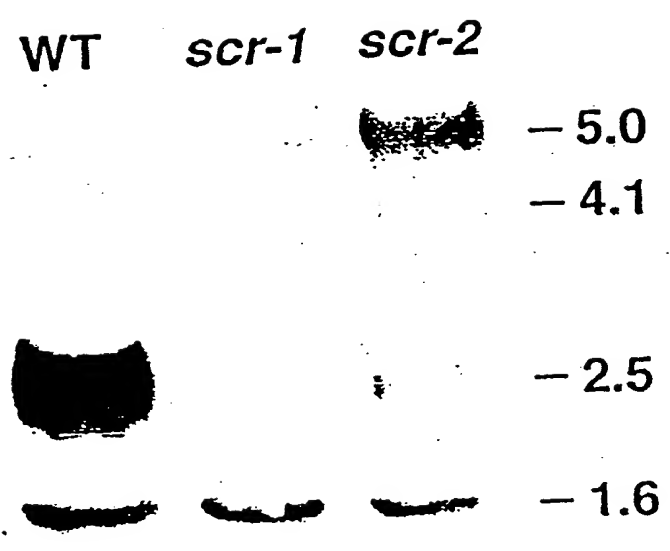


FIG. 6B

09265585.034099
6607ED" 98559260

A

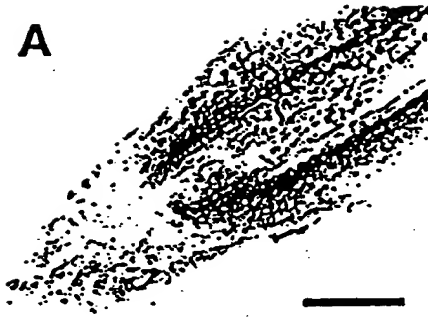


FIG. 7A

B



FIG. 7B



FIG. 7C

D

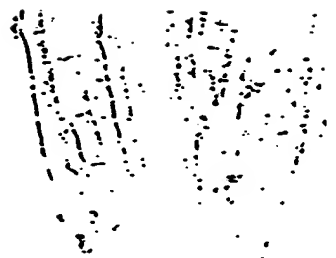


FIG. 7D

09265585.031099

E



FIG. 7E

F

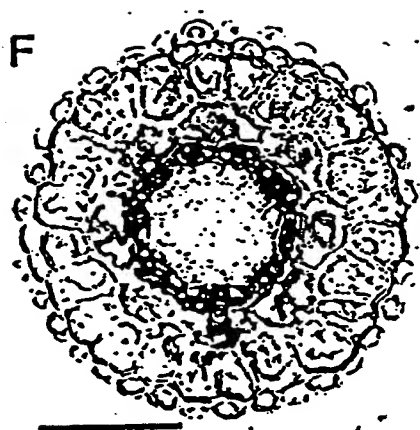


FIG. 7F

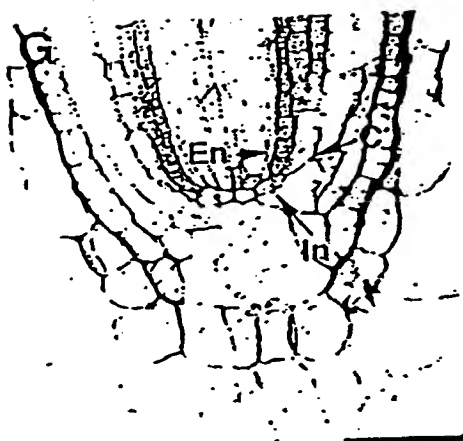


FIG. 7G

09265585 "031099

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GGCAGAGGC	CAACGGGIOC	TGAGCTICTT	ACTTATATGC	ATATCTTGTA	50
G T S P	T G P	E L L	T Y M H	I L Y	
TGAAGCCTGC	OCTTATTICA	AATTGCGTTA	TGAATCTGCT	AATGGAGCTA	100
E A C	P Y F K	F G Y	E S A	N G A I	
TAGCTGAAGC	TGIGAAGAAC	GAAAGTTTIG	TGCACATTAT	CGATTTCAG	150
A E A	V K N	E S F V	H I I	D F Q	
ATTICTCAAG	GTTGTCATG	GGTGAGTTTG	ATCGTGCTIC	TGGTGCTAG	200
I S Q G	G Q W	V S L	I R A L	G A R	
AACITGGTGA	CCTCGGAACG	TTAGGATAAC	GGGAATTGAT	GATCCGAGAT	250
P G G	P P N V	R I T	G I D	D P R S	
CATOGTTTGC	TOGICAAGGA	GGACTTGAGT	TAGTTGGACA	AAGACTTGGG	300
S F A	R Q G	G L E L	V G Q	R L G	
AAGCTAGCTG	AAATGTGCGG	TGTTCCGTTT	GAGTTCCATG	GAGCTGCTTT	350
K L A E	M C G	V P F	E F H G	A A L	
ATGCTGCAAG	GAAGTCGAAA	TOGAGAAGCT	AGGAGTTAGA	AATGGAGAAG	400
C C T	E V E I	E K L	G V R	N G E A	
CGCTCGGGGT	TAACTTCCCG	CTTGTTCTTC	ACCACATGOC	TGATGAGAGT	450
L A V	N F P	L V L H	H M P	D E S	
GTAACITGGG	AGATTCACAG	AGATAGATTG	TIGAGATTGG	TCAAACACTT	500
V T V E	N H R	D R L	L R L V	K H L	
GTCACCAAAC	GTTGTGACTC	TGGTTGAGCA	AGAAGCGAAT	ACAAACACTG	550
S P N	V V T L	V E Q	E A N	T N T A	
CGCCTTTTCT	TCCCGGTTT	GTCGAGACAA	TGAACCATTA	CTTGGCAGTT	600
P F L	P R F	V E T M	N H Y	L A V	

FIG. 8

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
TTCGAATCAA	TAGATGIGAA	ACTCGCTAGA	GATCACAAGG	AAAGGATCAA	650
F E S I	D V K	L A R	D H K E	R I N	
TGTTGAGCAG	CATTGTTTGG	CTAGAGAGGT	TGIGAATCTT	ATAGCTTIGG	700
V E Q	H C L A	R E V	V N L	I A C E	
AAGGTGTGTA	AAGAGAAGAG	AGGCAAGAGC	CACIAGGGAA	ATGGAGGICT	750
G V E	R E E	R H E P	L G K	W R S	
CGGTTTCACA	TGGGGGATT	TAAACGGTAT	CCTTTGAGCT	CGIATGIGAA	800
R F H M	A G F	K P Y	P L S S	Y V N	
CGCAACAATC	AAAGGATTGC	TTGAGAGTTA	TTCAGAGAAG	TATACACTTG	850
A T I	K G L L	E S Y	S E K	Y T L E	
AAGAAAGAGA	TGGAGCATTG	TATTTAGGAT	GGAAGAATCA	ACCTCTTATC	900
E R D	G A L	Y L G W	K N Q	P L I	
ACTTCTTIGG	CTTGGAGGTA	ACTAATAAAA	ACCTTGTTOG	GTTTCAGAAG	950
T S C A	W R X				
AGATTAGAAA	CTTCTTTTAA	AGTTTGCAGA	ATCTGTTTGT	AAAAGTAAAA	1000
CTCATGCATG	ATCGNAGGA	ACAAGTTGTC	AAATGTTGTA	GTAGTAAGTG	1050
ATATGTTGAT	GACCCAAAAA	AAAAAAAAAA	AAAAA		1085

Fig. 8 (cont'd.)

09265585-031099

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GCTATGGAAG	GAGAGAAGAT	GGTTCATGTG	ATTGATCTCG	ATGCTTCTGA	50
A M E G	E K M	V H V	I D L D	A S E	
GOCAGCTCAA	TGGCTTGCTT	TGCTTCAAGC	TTTAACTCT	AGGCTGAAG	100
P A Q	W L A L	L Q A	F N S	R P E G	
GTOCAOCTCA	TTTGAGAATC	ACTGGTGTTC	ATCACCAGAA	GGAAGTGCTT	150
P P H	L R I	T G V H	H Q K	E V L	
GAACAAATGG	CTCATAGACT	CATTGAGGAA	GCAGAGAAAC	TOGATATCCC	200
E Q M A	H R L	I E E	A E K L	D I P	
GTTTCAGTTT	AATCCCGTTG	TGAGTAGGTT	AGACTGTGTA	AATGTAGAAC	250
F Q F	N P V V	S R L	D C L	N V E Q	
AGTTGCGGGT	TAAACAGGA	GAGGCTTAG	CGGTAGCTC	GGTCTTCAA	300
L R V	K T G	E A L A	V S S	V L Q	
TTGCATACCT	TCTTGGCTC	TGATGATGAT	CTCATGAGAA	AGAACTGCGC	350
L H T F	L A S	D D D	L M R K	N C A	
TTTACGGTTT	CAGAACAACC	CTAGTGGAGT	TGACTTGCAG	AGAGTICTAA	400
L R F	Q N N P	S G V	D L Q	R V L M	
TGATGAGCCA	TGGCTCTGCA	GCTGAGGCAC	GTGAGAATGA	TATGAGTAAC	450
M S H	G S A	A E A R	E N D	M S N	
AACAATGGGT	ATAGCCCTAG	CGGTGACTCG	GCTCATCTT	TGCTTTTACC	500
N N G Y	S P S	G D S	A S S L	P L P	
AAGTTCAGGA	AGGACTGATA	GCTTCTCAA	TGCTATTGG	GGTTTGTCTC	550
S S G	R T D S	F L N	A I W	G L S P	
CAAAGGTCAT	GGTGGTCACT	GAGCAAGACT	CAGACCACAA	CGGCTCCACA	600
K V M	V V T	E Q D S	D H N	G S T	

Fig. 9

0026585-031099

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CTAATGGAGA	GGCTATTAGA	ATCACTTTAC	ACCTAAGCAG	CATIGTTTGA	650
L M E R	L L E	S L Y	T Y A	A L F D	
TIGCTTGGAA	ACAAAAGTTC	CAAGAAGTTC	TCAAGATAGG	ATCAAAGTGG	700
C L E	T K V P	R T S	Q D R	I K V E	
AGAAGATGCT	CTTGGGGGAG	GAGATCAAGA	ACATCATATC	CTGGGAGGGA	750
K M L	F G E	E I K N	I I S	C E G	
TTTGAGAGAA	GAGAAAGACA	CGAGAAGCTT	GAGAAATGGA	GCCAGAGGAT	800
F E R R	E R H	E K L	E K W S	Q R I	
CGATTGGCT	GGTTTGGGA	ATGTTCTCT	TAGCTATTAT	GCGATGTTCC	850
D L A	G F G N	V P L	S Y Y	A M L Q	
AGGCTAGGAG	ATTGCTTCAA	GGTGGGGT	TTGATGGGTA	TAGAATCAAG	900
A R R	L L Q	G C G F	D G Y	R I K	
GAAGAGAGCG	GGTGGGAGT	AATTGCTGG	CAAGATOGAC	CTCTATATCT	950
E E S G	C A V	I C W	Q D R P	L Y S	
GGTATCAGCT	TGGAGATGCA	GGAAGTGAAT	GATATATTAC	AGTTTGTCTT	1000
V S A	W R C R	K X			
CTATTTGGT	TATGAGCAGA	GTCCTTTCT	TTTTTGTATA	CATGGGGACA	1050
CAATCTTAGT	TGTTTGTGA	TGGTACCTT	CTGTCTCTTT	ATGCTATTTT	1100
GGCTTAAATG	CTTCTACTGC	CTCTGCATGT	AAAGCCTTTG	TGTGTGGTT	1150
CAATTGGTIC	TGGTGGGGT	GTAATAACAA	ACCAATCCA	ATTGAGCTG	1200
AAGATAACTA	ATTGATGAT	CGCTGTGTG	C		1231

FIG. 9 (cont'd.)

09265585, 031099

CTTTGTCAAT	GGTAAATGAG	CTGAGGCAGA	TAGTTTCTAT	CCAAGGAGAC	50
CCTTCTCAGA	GAATCGCAGC	TTACATGGTG	GAAGGTCTAG	CTGCAAGAAT	100
GGCCGCTTCA	GGAAAATTCA	TCTACAGAGC	ATTGAAATGC	AAAGAGCCTC	150
CTTCGGATGA	GAGGCTTGCA	GCTATGCAAG	TCCTGTTTGA	AGTCTGCCCT	200
TGTTTCAAGT	TCGGGTTTTT	AGCAGCTAAT	GGTGCGATAC	TTGAAGCAAT	250
CAAAGGTGAA	GAAGAAGTTC	ACATAATCGA	TTTCGATATA	AACCAAGGGA	300
ACCAATACAT	GACACTGATA	CGAAGCATTG	CTGAGTTGCC	TGGTAAACGA	350
CCTCGCCTGA	GGTTAACAGG	AATTGATGAC	CCTGAATCAG	TCCAACGCTC	400
CATTGGAGGG	CTAAGAATCA	TCAATCTAAG	ACTCGAGCAA	CTCGCAGAGG	450
ATAATGGAGT	ATCCTTCAAA	TTCAAAGCAA	TGCCTTCAAA	GACTTCGATT	500
GTCTCTCCAT	CAACACTCGG	TTGCAAACCA	GGAGAAACCT	TAATCAGTGA	550
ACTTTGCATT	CCAACCTTCA	CACATGCCTG	ACGAGAGTGT	CACAACAGTA	600
AACCAGCGGG	ACGAGCTACT	TCACATGGTC	AAAAGCTTAA	ACCCGCTTGT	650
CACGGTCGTT	GAACAAGACG	TGAACACAAA	CACTTCACCG	TTCTTTCCCA	700
GATTCATAGA	GGCTTACGAA	TACTACTCAG	CAGTTTTCGA	GTCTCTAGAC	750
ATGACACTTC	CAAGAGAAAG	CCAAGAGAGG	ATGAATGTAG	AAAGACAGTG	800
TCTCGCTAGA	GACATAGTCA	ACATTGTTGC	TTGCGAAGGA	GAAGAACGGA	850
TAGAGAGATA	CGAGGCTGCG	GGAAAATGGA	GAGCAAGGAT	GATGATGGCT	900
GGATTCAATC	CAAAACCAAT	GAGTGCTAAA	GTAACCAACA	ATATACAAAA	950
CCTGATAAAG	CAACAATATT	GCAATAAGTA	CAAGCTTAAA	GAAGAAATGG	1000
GTGAGCTCCA	TTTTTGCTGG	GAGGAGAAAA	GCTTAAATCGT	TGCTTCAGCT	1050
TGGAGGTAAG	ATAAGTGACA	AGAGCATATA	GTCTTTATGT	TTCATAAAAC	1100
ATAATTATGT	TTTTACTGTA	ATCTTGGGTT	ATTGTGTAAC	TGGTTAAATC	1150
ATCTCCATGT	ATTATTACCA	GAGGTTAGGG	GTGATCACAG	GTAATAAAAG	1200
CTAATCTAAC	ACTTATGGAA	GAATTTTTCT	TTCTTTTTTT	TCCCTATTAT	1250
ATAAAAATAA	TTAGAGTTTT	GGTTCTAAAC	CTATTTGCTA	AGTGTGAATG	1300
AGTCTTTACA	TGTTTCATATT	TCAGTTCAAA	TGGTTAAATT	TGTTAAGGTT	1350
CTCACTTAAA	AAAAAA				

Fig. 10

Zm-scl1

10	20	30	40	50
CCAGGAGGCGTTTCGAGCGGGAGGAGCGTGTGCACATCATCGACCTCGACA				
Q E A F E R E E R V H I I D L D I				
60	70	80	90	100
TCATGCAGGGGCTGCAGTGGCGGGCCTCTTCCACATCCTTGCCCTCCCGC				
M Q G L Q W P G L F H I L A S R				

FIG. 11 A

09265585-031099

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CCACGGCTCG	TCAAAGGATA	CAACCATGTA	CACATAATIG	ACTTTTCOCT	50
H A S V	K G Y	N H V	H I I D	F S L	
GATGCAAGGT	CTOCAGTGGC	CGGCACATCAT	GGATGICITC	TOOGOOOGIG	100
M Q G	L Q W P	A L M	D V F	S A R E	
AGGGTGGGOC	ACCAAGCTC	CGAATCACAG	GCATTGGGOC	GAACCCATA	150
G G P	P K L	R I T G	I G P	N P I	
GGTGGGOGIG	AOGAGCTCCA	TGAAGTGGGA	ATTGGGCTOG	CCAAGTATGC	200
G G R D	E L H	E V G	I R L A	K Y A	
ACACTGGTIG	GGTATOGACT	TCACITTCOA	GGGAGICTGT	GTOGATCAAC	250
H S V	G I D F	T F Q	G V C	V D Q L	
TTGATAGGTT	GTGGGACTGG	ATGCTTCTCA	AACCAATCAA	AGGAGAGGCA	300
D R L	C D W	M L L K	P I K	G E A	
GTGGCATAA	ACTOCATCCT	ACAACATCAT	OGCTCTCTOG	TIGACCCAGA	350
V A I N	S I L	Q L H	R L L V	D P D	
TGCAAACCCA	GTGGTGGGCG	CACCAATAGA	TATCTCTCTC	AAATTGGTCA	400
A N P	V V P A	P I D	I L L	K L V I	
TCAAGATAAA	CCCATGATC	TTCAAGGTTG	TIGAGCATGA	GGCAGATCAC	450
K I N	P M I	F T V V	E H E	A D H	
AACAGACCAC	CACTACTAGA	GAGGTTCACT	AATGGGCTCT	TCCACTATGC	500
N R P P	L L E	R F T	N A L F	H Y A	
GACCATGTTT	GACTCTTTGG	AGGOCATGCA	TGTTGTIACC	AGTGGTAGAG	550
T M F	D S L E	A M H	R C T	S G R D	
ACATCACCGA	CTCACACACA	GAGGTGTIACC	TTCGAGGIGA	GATTTTIGAC	600
I T D	S L T	E V Y L	R G E	I F D	

Fig. 11B

	10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
ATTGTCTGCG	GCGAGGGCAG	TGCAOGCACC	GAAOGICATG	AGTTGTTTGG		650
I V C G	E G S	A R T	E R H E	L F G		
TCACIGGAGG	GAGAGGCTCA	CCATATGCTGG	GCTAACTCAA	GTTGTGGTTGG		700
H W R	E R L T	Y A G	L T Q	V W F D		
ACCCCGATGA	GGTTGACACG	CTAAAAGACC	AGTTGATCCA	TGTGACATCC		750
P D E	V D T	L K D Q	L I H	V T S		
TTATCTGGCT	CTGGGTTCAA	CATCCTAGTG	TGTGATGGCA	GCCTTGCCT		800
L S G S	G F N	I L V	C D G S	L A L		
AGCGTGGCAT	AATOGCCCGT	TATATGTGGC	AACAGCTTGG	TGTGTGACAG		850
A W H	N R P L	Y V A	T A W	C V T G		
GAGGAAATGC	TGCCAGTTCC	ATGGTTGGCA	ACATCTGTAA	GGGTACAAAT		900
G N A	A S S	M V G N	I C K	G T N		
GATAGTAGAA	GAAAGGAAAA	CCGTAAATGA	CCCATGGAGT	AGCAGGAAGA		950
D S R R	K E N	R N G	P M E X			
ATAACCATGT	CATGAGCAAA	TGGATCAAGT	AATAAAATGC	ACTGATGACA		1000
TGCATGGTGA	TCTAAAGTTT	TTTIGGGTGA	ATGTGCAATG	ACGAATTGTT		1050
CAATTTGAAT	AACTAATCA	TGAGACTCAA	AAAAAAAAAA	AAA		1093

FIG. 11B (cont'd.)

CCCAACTTGG	GAAGCCCTTC	CTCCGCTCCG	CCTCCTACCT	CAAGGAGGCC	50
CTCCTCCTCG	CACTCGCCGA	CAGCCACCAT	GGCTCCTCCG	GCGTCACCTC	100
GCCGCTCGAC	GTTGCCCTCA	AGCTTGCAGC	ATACAAGTCT	TTCTCTGACC	150
TGTCACCTGT	GCTCCAGTTC	ACTAACTTTA	CCGCAACAAG	GCGCTTCTTG	200
ATGAGATTGG	TGGCATGGCA	ACTTCCTGCA	TCCATGTCAT	TGACTTTGAT	250
CTCGGTGTTG	GTGGTCAGTG	GGCTTCCTTC	TTGCAGGAGC	TTGCCCACCG	300
CCGGGGAGCT	GGAGGTATGG	CCITGCCGTT	GTTGAAGCTC	ACGGCTTTCA	350
TGTCGACTGC	TTCTCACCAT	CCACTGGAGC	TGCACCTTAC	CCAGGATAAC	400
CTCTCTCAGT	TTGCCGCAGA	GCTCAGAATT	CCTTTCGAAT	TCAATGCCGT	450
CAGTCTTGAT	GCATTCAATC	CTGCGGAATC	TATTTCTTCC	TCTGGTGATG	500
AAGTTGTTGC	TGTTAGCCTC	CCTGTTGGCT	GCTCTGCTCG	TGCACCACCG	550
CTGCCAGCGA	TTCTTCGGTT	GGTGAAACAG	CTTTGTCCTA	AGGTTGTCGT	600
GGCTATTGAT	C				

FIG. 12A

09265585.034099

096595.031099

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TACAGAGCAA	CAGCAGTATA	50
ATATTAATTC	TGTACCACAC	AACCATTGGA	TAGGTAAAT	TACCCTCTAG	100
TCTCTACTCA	TAAGCAGTGT	TTCCAATGAG	ATGATCATGG	CTAATTGAGC	150
AGAGCATGGC	AACAACCTAA	AGCAACATCA	TTAGCTATAG	AGACTGACAC	200
CAATATTCCT	AAATCCACTA	GGCTAGCTAA	TAAGCTGCAA	CGAAAAGCAA	250
TATGAAGAGT	TCAACAGCTC	AAGACAACAA	TTTCATTGTC	AACATTTAAT	300
TGCAAGAATA	AATGGACATT	ACTGGAGTGG	TCGATGCTTG	CAAACGGTGG	350
TGGAACCTTG	GTGGAGTGAA	GCTTATGGCT	GATCAGCACC	GCCAAGATGA	400
TATGGATACA	AGCTCCCCAC	GCTGCCAGTA	GAGCGTAAGA	GCAGCTCCGC	450
GTTTCTCCAC	ATGGAATCCT	CGGACCTGCA	CCCGCTTCAG	GAGGCAGTCT	500
GC					

FIG. 12B

FIG. 13A

SCR MAESGDFNGGQPPPHSPRLRTTSSGSSSSNNRGPPPPPPPLVMVRKR----LASEMSS
TF1 MKRD---HHQFQGRLSNHTSSSSSSISKD--MMVKKEEDGGCNMDELLAV-----
TF4 MKRDHHHHHQ-----DKKTMM--NEEDDGNGM-DELLAV-----

SCR |----- MOTIF I -----|
TF1 NPDYNNSSRPPRRVSHLLDSNYNTVTPQQPPSLTAAATVSSQPNPPLSVCGFSG
TF4 -LGKVRSSSEMAEVALKLEQLETMSNAQEDGLSHLATDAHYNPSELYS-----
-LGKVRSSSEMADVAQKLEQLEVMSNVQEDDLSQLATETVHYNPAELYT-----

SCR LPVFPSPDRGGRNVMMSVQPMDDSSSSSASPTVWVDAIRDLIHS---STSVSIPOL
TF1 -----WLDNMLSELNPPPLPASSNGLDPVL
TF4 -----WLDSMLTDLNPP---SSN-AEYDL

SCR IQNVRDIIFFPCNPNLGALLEYRLRLMLDPSSSSSDPSPQTTEPLYQISNNPSP
TF1 PSPEICGFPPXSDYDLKVI PXNAIYQPPAIDSSSSNN--Q-----
TF4 -----KAI-P-----GDILNQF-AIDSASSSN--Q-----

FIG. 13B

SCR
TF1
TF4
PQQQQHQQQQHKPPPIQQQERENSTDPQPPEVTATVPVQNTTAAE
-----NKRLKSSSPDSMTSTGTQIGGVIGTIVTTTTTTTAAAES
-----GGGDDTYTINKRLKCSNGVETTTATTAES

SCR
TF1
TF4
3898
----- MOTIF II (DIMERIZATION?) -----
LREKKEIKRQKQDEGLHLLTLLQCAEAVSADNLEANKLLLEISQLSTPYG
LSMVNELRQIVSIQ
-----TRSVILVDSQENGVRVLVHALMACAEAIQNNLTIAEALVKQIGCLAVSQ
-----TRHVVLVDSQENGVRVLVHALLACAFAVQENLTVAEALVKQIGFLAVSQI
QLGKPFLL

SCR
4818
1110
TF1
TF4
3989
-----|-----
TSAQRVAAYFSEAMSARLLNSCLGIYALPSRWMPQTHSLKMVSASFQVFNGISP
GTSPT-GPELLTYMHILYEACP
DPSQRIAAVMVEGLAARMAASGKFTYRAL-KCKEPPS--DEKLAAMQVLFVCP
GAMRKVATYFAEALARR-----IY-RL-SPQNQIDHCLSDTLQMHFYETCP
GAMRQVATYFAEALARR-----IY-RL-SPSQSPIDHSLSDTLQMHFYETCP
-----RSASYLKEALLLALADSHHGSSGV-T-SPLDVA-----LKLAAVKSFSDLSP

FIG. 13C

```

----- MOTIF III (VH1D) -----
SCR  LVKFSHTANQAIQEAFEK--EDSVHIIDLDIMQGLQWPGLFHILASRPGGP-----HVR
4818 YKFGVYESANGAIAEAVKN--ESFVHIIDFQISQGGQWVSLIRALGAPGPP-----NVR
1110 YKFGVYESANGAIAEAVKN--EEVHIIDFDINGNQYMTLIRSLAELPGKRP-----RLR
3935 CFKFGFLAANGAILEAIKG--EEVHIIDFDINGNQYMTLIRSLAELPGKRP-----HLR
TF1  AMEG--EKMVHVLDLDASEPQWLLALQAFNSRPEGPP-----TFR
TF4  YLKEFAHFTYANQAILLEAFEG--KKRVHVIDFSMNQGLQWPAALMQALALBPGGP-----VFR
3989 YLKEFAHFTYANQAILLEAFEG--KKRVHVIDFSMNQGLQWPAALMQALALBPGGP-----VFR
18310 YLKEFAHFTYANQAILLEAFEG--KKRVHVIDFSMNQGLQWPAALMQALALBPGGP-----VFR
Zm-Sc11 VLQFTNFTANKALLDEIGMATSCIHVIDENLGVGQWASFLQELAHRRGAGMALPLK
Zm-Sc12 HASVKG--YNHVHIIDFSLMQGLQWPAALMDVFSAREGGP-----KLR
Human  QEAER--EERVHIIDLDIMQGLQWPGLFHILASR
      FAG--CRRVHVDFGIKQGMQWPAALXDIAL
      GRNGRTL--WLGEGHIDLWPLQGLLSQGLQRAACARPLGAP-----HVF-

```

	--- ----- ----- -----	MOTIF	IV (DIMERIZATION)	----- ----- ----- -----	MOTIF	V
SCR	LTG LGTSMEA	LQATGKR	LSDFTDK	GLPFEECP	LAEKVGN	DLTERLNV
4818	ITGIDDPRSSFARQGG	LELVGQR	LGKLAEM	CGVPFEFHGA	LCCTEVEIEK	LGCV
1110	LTGIDDPESVQRSIGG	LRIINLR	LEQLAED	NGVSFKFKAM	PSKTSIVS	STLGC
3935	ITG VHQKEV	LEQMAHR	LIEBAEK	LDIPFQENPV	VSRLDCLN	VEQLRV
TF1	LTGIGPPAPDNSDH	LHEVGCK	LAQLAEA	IHVEFEYRGF	VANSIAD	LDASMLELRP
TF4	LTGIGPPAPDNFDY	LHEVGCK	LAHLAEA	IHVEFEYRGF	VANTLAD	LDASMLELRP
3989	LTAFMSTASHHPLE	LHLTQDN	LSQFAAE	LRIPEFN	AVSLDAFN	PAESISSGDE
18310	ITGIGPNPICGRDE	LHEVGIR	LAKYAHS	VGIDFTFQGV	CDVDQLDRL	CDWMLLKPI
Human	LPGLHTLS...	LGLQXRH	LLVHMMA	LSYSYGRXP...		

SCR	RKREA	VHMLQHS	LYDVTGSDA	HTLWLL	---QRLAPK	-----
4818	RNGEALAVN	EPPLV	LHMPDES	VTVENHR	---DRLRL	-----
1110	KPGETL	VNFAFQ	LHMPDES	VTVNQR	---DELHM	-----
3935	KTGEALAVS	SVLQ	HTFLASDD	ILMKNC	-ALRFQNN	PSGVDLQRYLMSHGS
TF1	SDTEAVAVN	SVFELH	KLGRG	KGIEKVLG	-----	-----
TF4	SEIESVAVN	SVFELH	KLGRG	KAIDKVLG	-----	-----
18310	K-GEAVAI	NSILQ	LHRLVDP	DANPVP	PAPIDILK	---
3989	VVAVSLPV	GC	SARAPPL	PAILRL	VKQLCPKVV	VAID

----- MOTIF VI -----

SCR VEQDLSHAGS--FLG-REVEAIIHYSALEFDSLGA SYGESE--ERHVEEQQ
4818 VEQEANTNTAP-FLP-RFVEETMNHYLAVFESIDVKLARDK--ERINVEQH
1110 VEQDVNTNTSP-FEP-RFIEAYEYYSAVFESLDMTLPRESQ--ERMNVERQ
3935 -EQSDSHNGS--TLMERLLESLTYTAALEFDCLETKVPTSQ--DRIKVEKM
TF1 XROEPNHNG-PGFLD-GXTESLHYSTXFDLEG--XPNSQ--DKLMSEXY
TF4 VEQESNHNS-PIFLD-RFTESLHYSTLFDLEG--VPSGQ--DKVMSEVY
18310 VEHEADHNR-PELLE-RFTNALFHYATMFDSL EAMHTCTSGRDI TDSLTEVY

FIG. 13F

SCR
4818 LLSKEIRNVLAVGSPSRSGEVKFE-SWREKMQCCGFKGIS-
1110 CLAREVNNLIACEGEVEREBRHEPLGKWSRFHMAGFKPYP-
3935 CLARDIVNIACEGEERIEREYEAAGKWRARMMAGFNPXP-
TF1 LFGEIKNIIISCEGFERREHEKLEKWSQRI DLAFGNVP-
TF4 -LGXQICNLVACEGPDVERHETLSQWGNRFGSSGLAPAH-
18310 -LGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAAAH-
-LRGEIFDIVCGESARTERHELFCHWRERLTYYAGLTQVWF

SCR
4818 LAGNATQATLLLGMPFS-DGYTLVDDN-GTLKLGKDL SLLTASAWTPRS*
1110 LSSYVNATIKGLEES-YS-EKYTL-EERDGA LYLGWKNQPLITSCAWR*
3935 MSAKVTTNNIÖNLIKQÖYC-NKYKLKEEM-GELHFCWEKSLIVASAWR*
TF1 LSYYAMLQARRLLQCGCF-DGYRIKEES-GCAVICWQDRPLYSVSAWRCRK*
TF4 LGSNAFKQASMLLSVFNSGQGYRV-EESNGCLMLGWHTRPLITSAWKLSTAAH*
3989 IGSNAFKQASMLLALFNGGEGYRV-EESDGCMLGWHTRPLIATSAWKLSTN*
18310 ADCLL-KRVQVRGFHV-EKRGALTLXWQRGELVSISSWRC*
DPDEVDTLKDQLIHVTSLSGSGFNILVCDGLALAWHNRP LYVATPAWCVTGNAA

18310 SSMVGNICKGTNDSRRKENRNGPME*

FIG. 14

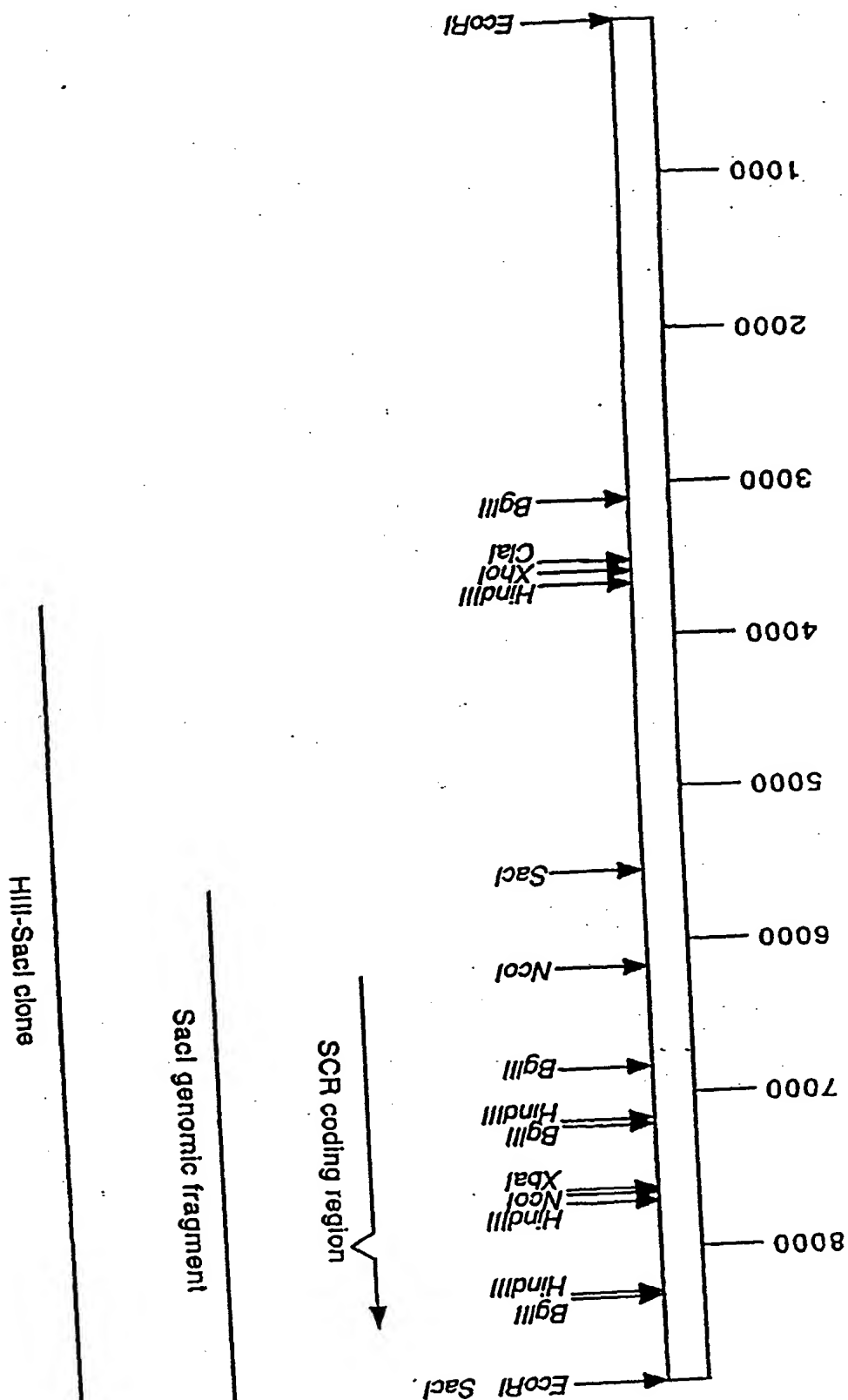


FIG. 15A

Old Name							New Name
Scr	SCR
3989	SRPo3
12398	SRPa6
4871	SRPa5
11846	SRPo4
2504	SRPo2
3935	SRPa3
11261	SRPa10
713	SRPo1
10964	SRPa9
23196LL	KVLLCHLVAE	STKRRIKIRP	LLDINDSGFL	GFWSWIHMGS	SRPa12
Tf1	SRPa8
Tf4	SRPa2
18310	SRPm1
18652	SRPa11
4818	SRPa4
21729	SRPa7
1110	SRPa1
174	SRPb1
33/08	SRPa13
-150							-101

09265585.031099

FIG. 15B

Scr
3989
12398
4871
11846
2504
3935
11261
713
10964
23196	YPDGFFGSMD	ELDFNKDFDL	PPSSNQTLGL	ANGFYLDDDL	FSSLDPPEAY
Tf1
Tf4
18310
18652
4818
21729
1110
174
33/08
-100					-51

FIG. 15D

Scr	MAESGDFNGG	QPPPHSPLRT	TSSGSSSSNN	RGPPPPPPPP	LVMVRKRLAS
3989
12398
4871
11846
2504
3935
11261
713
10964
23196	CMFHDALALQ	AAEKSLEYAL	GEKDPSSSSA	SSVDHPERLA	SHSPDGSCSG
Tf1
Tf4
18310
18652
4818
21729
1110
174
33/08TSDSA	SSFNIPTSAQ	NHYATGSFST
1					50

FIG. 15E

	←-----Motif I -----→				
Scr	EMSSNPDYNN	SSRPFRVSH	LLDSNYNTVT	PQQPPSLTAA	ATVSSQPNPP
3989
12398
4871
11846
2504
3935
11261
713
10964
23196	GAFSDYASTT	TTTSSDSHWS	VDGLENRPSW	LHTPMPSNFV	FQSTSRNSNV
Tf1MKRDHHQFQ	GRLSNHGTSS	SSSSISKDKM	MMVKKEEDGG
Tf4MKRDHHHHHQDKK	TMMNEEDDG
18310
18652
4818
21729
1110
174
33/08	NSRTTNVATA	TTNSATAHWV	ATDAEHTDTI	IAQP	
	51				100

660FE0"58559260

FIG. 15F

Scr	LSVCGFSGLP	VFPSDRGGRN	VMMSVQPMDO	DSSSSSASPT	VWVDARIIDL
3989
12398
4871
11846
2504
3935
11261
713
10964
23196	TGGGGGGNSA	VYSGFGDDL	VSNMFKDDEL	AMQFKKGVEE	ASKFLPKSSQ
Tf1	GNMDELLAV	LGYKVRSEM	AEVALKLEQL	ETMMSNAQED	GLSHLATDAA
Tf4	NGM.DELLAV	LGYKVRSEM	ADVAQKLEQL	EVMSNVQED	DLSQLATETV
18310
18652
4818
21729D
1110
174
101					150

092655-031099

FIG. 15G

Scr	IHSSTSVSIP	QLIQNVRDII	FPCNPNLGAL	LEYRLRSLML	LDPSSSSDPS
3989
12398
4871
11846
2504
3935
11261
713
10964
23196	LFIDVDSYIP	MNSGSKENG	EVFVKTEK	ETEHHHHHSY	APPPNRLTGK
Tf1	HYNPSELYSW	LDNMLSELNP	PPLPASSNGL	DPVLPSPEIC	GFPXSDYDLK
Tf4	HYNPAELYTW	LDSMLTDLNP	P....SSNA.EYDLK
18310
18652
4818
21729	LTSVNDMSLF	GGSGSSQRYG	LPVPRSQTQQ	QQSDYGLFGG	IRMGIGSGIN
1110
174
151					200

FIG. 15H

Scr	PQTFEPLYQI	SNNPSPPQQQ	QQHQQQQQQH	KPPPPPIQQQ	ERENSSTDAP
3989
12398
4871
11846
2504
3935
11261
713
10964
23196	KSHWRDEDED	VEERSNKQSA	VYVEESEELSE	MFDNMFLOGP	GKPVCILNQ
Tf1	VIPXNAIYQF	PAIDSSSSSN	NQ.....	NKRLKSCSSP	DSMVTSTSTG
Tf4	AIPGDAILNQ	FAIDSASSSN	QGGGGDTYTT	NKRLKCS...
18310
18652
4818
21729	NYPTLTGVPC	IEPVQNRVHE	SENMLNSLRE	LEKQLLDDDD	ESGGDDDVSV
1110
174
201					250

FIG. 15I

		←-- bZIP like domain →--				
		←-- Motif II (dimerization) →--				-----
Scr	PQPETVTATV	PAVQTNTAEA	LRERKEEIKR	QKQDEEGLHL	LTLLLQCAEA	
3989	
12398	
4871AAIFYG	HHHHTPPPAK	RLNPGPVGIT	
11846	
2504	
3935	
11261	
713	
10964	
23196	NFPTESAKVV	TAQSNQAKIR	GKKSTSTSHS	NDSKKETADL	RTLLVLCQA	
Tf1	TQIGGVIGTT	TTTTTTTTTA	AAESTRSVIL	VDSQENGVR	VHALMACAEA	
Tf4	...NGVVE..TTTA	TAESTRHVVL	VDSQENGVR	VHALLACAEA	
18310	
18652	
4818	
21729	ITNSNSDWIQ	NLVTPNPNPN	PVLSFSPSSS	SSSSSPSTAS	TTTSVCSRQT	
1110	
174	
251					300	

09065585.031099

FIG. 15J

	----- Motif II (dimerization) ----->				
Scr	VSADNLEEAN	KLLLEISQLS	TPYGTSAQRV	AAYFSEAMSA	RLSNSCLGIY
3989
12398
4871	EQLVKAAEVI	ESDTCLAQGIL	ARLNQQLSS	PVGKPLERAA	FYFKEALNNL
11846
2504
3935
11261
713
10964
23196	VSVDDRRRTAN	EMLRQIREHS	SPLGNGSERL	AHYFANSLEA	RLAGTGTQIY
Tf1	IQQNNLTLAE	ALVKQIGCLA	VSQAGAMRKV	ATYFAEALAR	RIYRLSPPQN
Tf4	VQKENLTVAE	ALVKQIGFLA	VSQIGAMRQV	ATYFAEALAR	RIYRLSPSQS
18310
18652
4818GT
21729	VMEIATAIAE	GKTEIATEIL	ARVSQTPNLE	RNSEEKLVDF	MVAALRSRIA
1110	...LSMVNEL	RQIVSIQGD	SQRIAAVMVE	GLAARMAASG	KFIYRALKCK
174
301					350

09265585.031099

FIG. 15K

	Scr	AALPSRWMPQ	THSLKMVSFA	QVFNGISPLV	KFSHFTANQA	IQEAFEKEDS
3989LYRNKALL	DEIGGMATSC
12398
4871	LHNVSQTLA	CSLIFKVAAY	KSFSEISPVL	QFANFTSNQA	LLESFHGFHR	
11846
2504
3935AMEGEKM
11261
713
10964
23196	TALS...SKK	TSAADMLKAY	QTYMSVCPFK	KAATIFANHS	MMRFTANANT	
Tf1	QIDHCLSDT.LQ	MHFYETCPYL	KFAHFTANQA	ILEAFEGKKR	
Tf4	PIDHSLSDT.LQ	MHFYETCPYL	KFAHFTANQA	ILEAFQGKKR	
18310HA	SVKGYN...H	
18652ANVE	ILEAIAGETR	
4818	SPTGPELLT.YM	HILYEACPYF	KFGYESANGA	IAEAVKNESF	
21729	SPVTELYGKE	HLISTQL...	..LYELSPCF	KLGFEEANLA	ILDAADNNDGGMMI	
1110	EPPSDERLA.AM	QVLFEVCPCF	KFGFLAANGA	ILEAIKGEEE	
174	
351						400

← Motif III (SCR VHIID) →

09265585-031099

FIG. 15L

```

-- Motif III (VHIID) -----|< -- Motif IV ---
Scr VHIIDLDIMQ GLQWPGLFHI LASRPGGPPH VRLTGLGTSM EA.....LQ
3989 IHVIDFDLGV GGQWASFLQE LAHRRGAGGM ALPLLKLTAF MSTASHHPLE LH
12398 .....
4871 LHIIDFDIGY GGQWASLMQE LVLRDNAAPLSLKITVFASPA NHVQLELG..
11846 .....
2504 .....
3935 VHVIDLDASE PAQWLALLQA FNSRPEGPPH LRITGVHHQK EVLE.....
11261 .....
713 .....
10964 .....
23196 IHIIDFGISY GFQWPALIHRLSLSRPGGSPK LRITGIELPQ RGFRPAE...
Tf1 VHVIDFSMNQ GLQWPALMQA LALREGGPPT FRLTGIGPPA PDNSDHLH..
Tf4 VHVIDFSMSQ GLQWPALMQA LALRPGGPPV FRLTGIGPPA PDNFDYLH..
18310 VHIIDFSLMQ GLQWPALMDV FSAREGGPPK LRITGIGPNP IGGRDELH..
18652 VHIIDFQIAQ GSQYMFLIQE LAKRPGG... ...PPLLRTV GVDDSQSTYARGGGLS
4818 VHIIDFQISQ GGQWVSLIRA LGARPGG... ...PPNVRT GIDDPRSSFARQGGLE
1110 VHIIDFDINQ GNQYMTLIRS IAELPGK... ...RPRLRLT GIDDPESVQRSIGGLR
21729 PHVIDFDIGE GGQYVNLRLT LSTRNGKSQ SQNSPVVKIT AVANNVYGDCLVDDGGEERLK
174 .....
401 .....
450

```

09265585 031099

FIG. 15M

	← --- Motif V ---→				
	--- Motif IV ---				
Scr	ATGKRLSDFT	DKLGLPFEFC	PLAEKVGNDL	TERLNVKRE	AVAVHWL...
3989	LHLTQDNLSQ	FAAELRIPFE	FNAVSLDAFN	PAESISSSGD	EVVAVSL...
12398
4871	FTQDNLKHFA	SEINISLDIQ	VL..SLDLLG	SISWPNSS..	EKEAVAVNIS
11846
2504NGGAF	APSTWTA...
3935	QMAHRLIEEA	EKLDIPFQFN	PVVSRLDCLN	VE...QLRVK	TGEALAVSSV
11261K	KWETITLDEL	MINPGETTVV
713
10964
23196	EFRRQVIAWL	DTVSDTMFRL	STTQLLRNGE	TIQVEDLKL	QGEYVVVNSL
Tf1	EVGCKLAQLA	EAIHVEFEYR	GFVANSLADL	DASMLELRPS	DTEAVAVNSV
Tf4	EVGCKLAHLA	EAIHVEFEYR	GFVANTLADL	DASMLELRPS	EIESVAVNSV
18310	EVGIRLAKYA	HSVGDFTFQ	GVCVDQLDRL	CDWML.LKPI	KGEAVAINSI
18652	LVGERLATLA	QSCGVPFEFH	D...AIMSGC	KVQREHLGLE	PGFAVVVNF
4818	LVGQRLGKLA	EMCGVPFEFH	G...AALFCT	EVEIEKLGVR	NGEALAVNFP
21729	AVGDLLSQLG	DHSISVSFNV	V...TSLRLG	DLNRESLGCD	PDETLAVNLA
1110	IIGLRLEQLA	EDNGVSFKFK	A...MPSKTS	IVSPSTLGCK	PGETLIVNFA
174
451	500

0965585.031099

FIG. 15N

----- Motif V -----					
Scr	...QHS....
3989P VG.....
12398
4871AA....
11846
2504R SL.....
3935	LQLHTFLASD	DDLMRKNCAL	RFHNNPSGVD	LQRVLMMSHG	SAAEARENDM
11261	NCIHRLQYTP	DE.....
713
10964
23196	FRFRNLL... DE.....
Tf1	FELHKLLGRX	GG.....
Tf4	FELHKLLGRP	GA.....
18310	LQLHRLLVDP	DA.....
18652	YVLHHM...P DE.....
4818	LVLHHM...P DE.....
21729	FKLYRV...P DE.....
1110	FQLHHM...P DE.....
174
501					550

0926585 "031099

FIG. 150

	Motif V ----->			<--- Motif VI ---	
ScrLYDVTGSD	AHTLWLLQRL	APKVVTVVEQ	DLSHAGS.FL	
3989CSARAPPL	PAILRLVKQL	CPKVVVAIDH	GGDRADLPFS	
12398	
4871SFSHLPLV	LRFVKHLSPT	IIVCSDRGCE	RTDLPFSQQL	
11846Q	EADHNKTGFL	
2504	.NGGAFAPST	WTARSLPVPSSPST	DSF.....	
3935	SNNNGYSPSG	DSASSLPLPSSGRT	DSFLNAIWGL	SPKVMVTEQ	DSDHNGSTLM
11261TVSLDSPR	DTVLKLFRDI	NPDLFVFAEI	NGMYNSPFFM	
713	NGSYNAPFFV	
10964AYNAPFFV	
23196TVLVNSPR	DAVLKLIRKI	NPNVFIPAIL	SGNYNAPFFV	
Tf1I	EKVLGVVKQD	TGDFHXWKRO	EPNHNGPGFL	
Tf4I	DKVLGVVNQI	KPEIFTVVEQ	ESNHNSPIFL	
18310NPVVPAPI	DILLKLVIKI	NPMIFTVVEH	EADHNRPELL	
18652SVSVEKYR	DRLLHLIKSL	SPNLVTLVEQ	EDNTNTSPLV	
4818SVTVENHR	DRLLRLVKHL	SPNVVTLVEQ	EANTNTAPFL	
21729SVCTENPR	DELLRRVKGL	KPRVVTLVEQ	EMNSNTAPFL	
1110SVTTVNQR	DELLHMVKSL	NPKLVTVVEQ	DVNTNTSPFF	
174	
	551			600	

096555 031099

FIG. 15P

```

----- Motif VI -----
Scr GRFVEAIHYY SALFDSLGA Y..GESEER HVVEQQLSK EIRNVLA VGG
3989 QHFLNCFQSC VFLDSLDAAG I..DADSA.. CKIERFLIQP RVEDAVIG..
12398 .....SLEPN L..DRDSKER LRVERVLFG RIMDLVRSDD
4871 AHSLSHTAL FESLDAVNAN L..DAM.... QKIERFLIQP EIEKLVLD..
11846 DRFTEALFYY SAVFDSLDA N..NNNNNNN QRMEA EYLQR EICDIVCGEG
2504 .....
3935 ERLLSLEYTY AALFDCLETK V..PRTSQDR IKVEKMLFGE EIKNIISCEG
11261 TRFREALFHY SSLFDMFDTT IHADEYKNR SLLERELLVR DAMRVISCEG
713 TRFREALFHY SAIFDMLETN I..PKDNEQR LLIESALFSR E.XNVISCEG
10964 TRFREALFHF SSIFDMLETI V..PREDEER MFLEMEVFGR EALNVIACEG
23196 TRFREALFHY SAVFDMCD SK L..AREDEMR LMYVFEFYGR EIVNVVASEG
Tf1 DGXTESLHYY STXFDSLEGX ...PNSQD.. KLMSEXYLGX QICNLVACEG
Tf4 DRFTESLHYY STLFD SLEGV ...PSGQD.. KVMSEVYL GK QICNVVACDG
18310 ERFNALFHY ATMFD SLEAM HRCTSGRDIT DSLTEVYLRG EIFDIVCGEG
18652 SRFVETLDYY TAMFESIDAA R..PRDDKQR ISAEQHCVAR DIVNMIACEE
4818 PRFVETMNH Y LAVFESIDVK L..ARDHKER INVEQHCLAR EVENLIACEG
21729 GRVSESCACY GALLESVEST V..PSTNSDR AKVE.EGIGR KLVNAVACEG
1110 PRFIEAYEYY SAVFESLDM T L..PRESQER MNVERQCLAR DIVNIVACEG
174 ..... .RXFDSLEHD A..SKGEPRE DERGRXCLAR NIVNIVXCKX
601 650

```

09265585.031099

FIG. 15Q

Scr	PSRSGEVKF.ESWRE	KMQQCGFKGI	SLAG..NAAT	QATLLLGMP
3989	.RHKA..Q..	...KAIWRS	VFAATGFKPV	QLSN..LAEA	QADCLLKRVO
12398	DNNKPGTRFG	LMEEKEQWRV	LMEKAGFEPV	KPSN..YAVS	QAKLLLNYN
4871	.RSRPIER..	...PMMTWQA	MFLQMGFSPV	THSN..FTES	QAECLVQRTF
11846	AARXERHE..	...PLSRWRD	RLTRAGLSAV	PLG....SNA
2504
3935	FERRERHE..	...KLEKWSQ	RIDLAGFGNV	PLSY..YAML	QARRLLQCGG
11261	AERFARPE..	...TYKQWRV	RILRAGFKPA	TIS....KQI	MKEAKEIVRK
713	LERMERPE..	...TYKQWQV	RNQRVGFKQL	PLN....QDM	MKRARKEGQV
10964	WERVERPE..	...TYKQWHV	RAMRSGLVQV	PFD....PSI	MKTSLSHKVHT
23196	TERVESRE..	...TYKQWQA	RLIRAGFRQL	PLE....KEL	MONLKLKIEN
Tf1	PDRVERHE..	...TLSQWGN	RFGSSGLAPA	HLGS...NAF	KQASMLLSVF
Tf4	PDRVERHE..	...TLSQWRN	RFGSAGFAAA	HIGS...NAF	KQASMLLALF
18310	SARTERHE..	...LFGHWRE	RLTYAGLTQV	WFDPEVDTL	KDQLIHVTSL
18652	SERVERHE..	...VLGKWRV	RMMAGFTGW	PVSTSAAFAA	SE....MLK.
4818	VEREERHE..	...PLGKWS	RFHMAGFKPY	PLSSYVNATI	KG....LLE.
21729	IDRIERCE..	...VFGKWRM	RMSMAGFELM	PLSEKIAESM	KS....RGNR
1110	EERIERYE..	...AAGKWRA	RMMAGFNPK	PMSAKVTNNI	QN....LIKQ
174	EERIERYE..	...VTGKWRA	RMMAGFSR	PMSGRVTSNI	ES....LIKQ
	651				700

09265585, 031099

FIG. 15R

	----- Motif VI ----->				
Scr	.SDGYTLVD.	DNGTLKLGWK	DLSLLTASAW	TPRSX.....
3989	VRGFH..VEK	RGAAALTLYWQ	RGELVSISSW	RCX.....
12398	YSTLYSLVES	EPGFISLAWN	NVPLLTVSSW	RX.....
4871	VRGFH..VEE	KHNSLLLCWQ	RTELVGVSAW	RCRSSX....
11846
2504
3935	FDGYR..IKE	ESGCAVICWQ	DRPLYSVSAW	RCRKX.....
11261	RYHRDFVIDS	DNNWMLQGWK	GRVIYAFSCW	KPAEKFTNNN	LNIX.....
713	LPTRTFIIDE	DNRWLLQGWK	GRILFALSTW	KPDNRSSSX.
10964	FYHKDFVIDQ	DNRWLLQGWK	GRTVMALSVW	KPESX.....
23196	GYDKNFDVDQ	NGNWLLQGWK	GRIVYASSLW	VPSSSX....
Tf1	NSGQGYRVEE	SNGCLMLGWH	TRPLITTSAW	KLSTAAHX..
Tf4	NGGEGYRVEE	SDGCLMLGWH	TRPLIATSAW	KLSTNX....
18310	.SGSGFNILV	CDGSLALAWH	NRPLYVATAW	CVTGGNAASS	MVGNICKGTN
18652	AYDKNYKLGG	HEGALYLFWK	RRPMATCSVW	KPNPNYIGX.
4818	SYSEKYTLEE	RDGALYLGWK	NQPLITSCAW	RX.....
21729	VHPG.FTVKE	DNGGVCFGWM	GRALTVASAW	RX.....
1110	QYCNYKLKE	EMGELHFCWE	EKSLIVASAW	RX.....
174	DYCSKYKVKE	EMGELHFSWE	EKSLIVASAW	SX.....
701					750

09265585.031099

FIG. 15S

Scr
3989
12398
4871
11846
2504
3935
11261
713
10964
23196
Tf1
Tf4
18310	DSRRKENRNG	PMEX
18652
4818
21729
1110
174

751

764

FIG. 16A

SRPa1 (1110)

CTTTGTCAATGGTAAATGAGCTGAGGCAGATAGTTTCTATCCAAGGAGACCCTTCTCAGA
GAATCGCAGCTTACATGGTGGGAAGGTCTAGCTGCAAGAATGGCCGCTTCAGGAAAATTCA
TCTACAGAGCATTGAAATGCAAAGAGCCTCCTTCGGATGAGAGGCTTGCAGCTATGCAAG
TCCTGTTTGAAGTCTGCCCTTGTTTCAAGTTCGGGTTTTTTAGCAGCTAATGGTGCGATAC
TTGAAGCAATCAAAGGTGAAGAAGAAGTTCACATAATCGATTTTCGATATAAAACCAAGGGA
ACCAATACATGACACTGATACGAAGCATTGCTGAGTTGCCTGGTAAACGACCTCGCCTGA
GGTTAACAGGAATTGATGACCCTGAATCAGTCCAACGCTCCATTGGAGGGGCTAAGAATCA
TCGGTCTAAGACTCGAGCAACTCGCAGAGGATAATGGAGTATCCTTCAAATTCAAAGCAA
TGCCTTCAAAGACTTCGATTGTCTCTCCATCAACACTCGGTTGCAAACCAGGAGAAACCT
TAATAGTGAACTTTGCATTCCAACCTCACCACATGCCTGACGAGAGTGTCAACACAGTAA
ACCAGCGGGACGAGCTACTTCACATGGTCAAAAGCTTAAACCCAAAGCTTGTCACGGTCG
TTGAACAAGACGTGAACACAAACACTTCACCGTTCTTCCCAGATTCATAGAGGCTTACG
AATACTACTCAGCAGTTTTTCGAGTCTCTAGACATGACACTTCCAAGAGAAAGCCAAGAGA
GGATGAATGTAGAAAGACAGTGTCTCGCTAGAGACATAGTCAACATTGTTGCTTGCGAAG
GAGAAGAACGGATAGAGAGATACGAGGCTGCGGGAAAATGGAGAGCAAGGATGATGATGG
CTGGATTCAATCCAAAACCAATGAGTGCTAAAGTAACCAACAATATACAAAACCTGATAA
AGCAACAATATTGCAATAAGTACAAGCTTAAAGAAGAAATGGGTGAGCTCCATTTTTTGCT
GGGAGGAGAAAAGCTTAATCGTTGCTTCAGCTTGGAGGTAAGATAAGTGACAAGAGCATA
TAGTCTTTATGTTTCATAAAACATAATTATGTTTTTACTGTAATCTTGGGTATTTGTGTA
ACTGGTTAAATCATCTCCATGTATTATTACCAGAGGTTAGGGGTGATCACAGGTACTAAA
AGCTAATCTAACACTTATGGAAGAATTTTTCTTTCTTTTTTTTCCCTATTATATAAAAAT
AATTAGAGTTTTGGTTCTAAACCTATTTGCTAAGTGTGAATGAGTCTTTACATGTTTATA
TTTCAGTTCAAATGGTTAAATTTGTTAAGGTCTCACTTAAAAA

FIG. 16B

SRPa3 (3935)

GCTATGGAAGGAGAGAAGATGGTTCATGTGATTGATCTCGATGCTTCTGAGCCAGCTCAA
TGGCTTGCTTTGCTTCAAGCTTTTAACTCTAGGCCTGAAGGTCCACCTCATTTGAGAATC
ACTGGTGTTTCATCACCAGAAGGAAGTGCTTGAACAAATGGCTCATAGACTCATTGAGGAA
GCAGAGAAACTCGATATCCCGTTTCAGTTTAATCCCGTTGTGAGTAGGTTAGACTGTTTA
AATGTAGAACAGTTGCGGGTTAAACAGGAGAGGCCCTTAGCCGTTAGCTCGGTTCTTCAA
TTGCATACCTTCTTGGCCTCTGATGATGATCTCATGAGAAAGAACTGCGCTTTACGGTTT
CAGAACAACCCTAGTGGAGTTGACTTGACAGAGAGTTCTAATGATGAGCCATGGCTCTGCA
GCTGAGGCACGTGAGAATGATATGAGTAACAACAATGGGTATAGCCCTAGCGGTGACTCG
GCCTCATCTTTGCCTTTACCAAGTTCAGGAAGGACTGATAGCTTCCTCAATGCTATTTGG
GGTTTGTCTCCAAAGGTCATGGTGGTCACTGAGCAAGACTCAGACCACAACGGCTCCACA
CTAATGGAGAGGCTATTAGAATCACTTTACACCTACGCAGCATTGTTTGATTGCTTGGAA
ACAAAAGTTCCAAGAACGTCTCAAGATAGGATCAAAGTGGAGAAGATGCTCTTCGGGGAG
GAGATCAAGAACATCATATCCTGCGAGGGATTTGAGAGAAGAGAAAGACACGAGAAGCTT
GAGAAATGGAGCCAGAGGATCGATTTGGCTGGTTTTGGGAATGTTCTCTTAGCTATTAT
GCGATGTTGCAGGCTAGGAGATTGCTTCAAGGGTGGGTTTTGATGGGTATAGAATCAAG
GAAGAGAGCGGGTGCGCAGTAATTTGCTGGCAAGATCGACCTCTATACTCGGTATCAGCT
TGGAGATGCAGGAAGTGAATGATATATTACAGTTTGTCTTCTATTTTGGTTATGAGCAGA
GTCCCTTTCTTTTTTGTATACATGGGGACACAATCTTAGTTGTTTTGTGATGGTGACTTT
CTGTCTCTTTATGCTATTTTGGCTTAAATGCTTCTACTGCCTCTGCATGTAAAGCCTTG
TGTGTTGGTTCAATTTGGTCTGGTGTGGGTGTAATACCAAACCAATCCAATTTGAGCTG
AAGATAACTAATTTGATGATCGGCTCGTGCC

09265585.031099

FIG. 16C

SRPa4 (4818)

GGCACGAGCCCAACGGGTCTGAGCTTCTTACTTATATGCATATCTTGTATGAAGCCTGC
CCTTATTTCAAATTCGGTTATGAATCTGCTAATGGAGCTATAGCTGAAGCTGTGAAGAAC
GAAAGTTTTGTGCACATTATCGATTTCCAGATTTCTCAAGGTGGTCAATGGGTGAGTTTG
ATCCGTGCTCTTGGTGCTAGACCTGGTGGACCTCCGAACGTTAGGATAACGGGAATTGAT
GATCCGAGATCATCGTTTGCTCGTCAAGGAGGACTTGAGTTAGTTGGACAAAGACTTGGG
AAGCTAGCTGAAATGTGCGGTGTTCCGTTTGAGTTCCATGGAGCTGCTTTATGCTGCACG
GAAGTCGAAATCGAGAAGCTAGGAGTTAGAAATGGAGAAGCGCTCGCGGTTAACTTCCCG
CTTGTTCTTCACCACATGCCTGATGAGAGTGTAAGTGTGGAGAATCACAGAGATAGATTG
TTGAGATTGGTCAAACACTTGTCAACAAACGTTGTGACTCTGGTTGAGCAAGAAGCGAAT
ACAAACACTGCGCCGTTTCTTCCCCGGTTTGTGCGAGACAATGAACCATTACTTGGCAGTT
TTCGAATCAATAGATGTGAAACTCGCTAGAGATCACAAGGAAAGGATCAATGTTGAGCAG
CATTTGTTTGGCTAGAGAGGTTGTGAATCTTATAGCTTGTGAAGGTGTTGAAAGAGAAGAG
AGGCACGAGCCACTAGGGAAATGGAGGTCTCGGTTTCAATGGCGGGATTAAACCGTAT
CCTTTGAGCTCGTATGTGAACGCAACAATCAAAGGATTGCTTGAGAGTTATTCAGAGAAG
TATACACTTGAAGAAAGAGATGGAGCATTGTATTTAGGATGGAAGAATCAACCTCTTATC
ACTTCTTGTGCTTGGAGGTAACATAAAAAACCTTGTTCGGTTTCAGAAGAGATTAGAAA
CTTCTTTTAAAGTTTGCAGAATCTGTTTGTAAAAGTAAAACTCATGCATGATCCGNAGGA
ACAAGTTGTCAAATGTTGTAGTAGTAAGTGATATGTTGATGACCCAAAAAAAAAAAAAA
AAAAA

0926555-031099

FIG. 16D

SRPa5 (4871)

GCGGCTATCTTCTACGGCCACCACCACCATACACCTCCGCCGGCAAAGCGGCTCAACCCT
GGTCCCGTGGGGATAACAGAGCAGCTGGTTAAGGCAGCAGAGGTCATAGAGAGCGACACG
TGTCTAGCTCAGGGGATATTGGCGCGGCTCAATCAACAGCTCTCTTCTCCCGTCGGGAAG
CCATTAGAAAGAGCAGCTTTTTACTTCAAAGAAGCTCTCAATAATCTCCTTCACAACGTC
TCCCAAACCCCTAAACCCTTATTCCCTCATCTTCAAGATCGCTGCTTACAAATCCTTCTCA
GAGATCTCTCCCGTTCTTCAGTTCGCCAACTTTACCTCCAACCAAGCCCTCTTAGAGTCC
TTCCATGGCTTCCACCGTCTCCACATCATCGACTTCGATATCGGCTACGGTGGCCAATGG
GCTTCCCTCATGCAAGAGCTTGTTCTCCGCGACAACGCCGCTCCTCTCTCCCTCAAGATC
ACCGTTTTTCGCTTCTCCGGCGAACCACGACCAGCTCGAACTTGGCTTCACTCAAGACAAC
CTCAAGCACTTCGCCTCTGAGATCAACATCTCCCTTGACATCCAAGTTTTGAGCTTAGAC
CTCCTCGGCTCCATCTCGTGGCCTAACTCGTCGGAGAAAGAAGCTGTCGCCGTAAACATC
TCCGCCCGCTCCTTCTCGCACCTCCCTTTGGTCCTCCGTTTCGTGAAGCATCTATCTCCG
ACGATCATCGTCTGCTCCGACAGAGGATGCGAGAGGACGGATCTGCCCTTCTCTCAACAG
CTCGCCCACTCGCTGCACTCACACACCGCTCTCTTGAATCCCTCGACGCCGTCAACGCC
AACCTCGACGCAATGCAGAAGATCGAGAGGTTTCTTATACAGCCGGAGATAGAGAAGCTG
GTGTTGGATCGTAGCCGTCCGATAGAAAGGCCGATGATGACGTGGCAAGCGATGTTTCTA
CAGATGGGTTTCTCACCGGTGACGCACAGTAACTTCACGGAGTCTCAAGCCGAGTGTTTA
GTCCAACGGACGCCAGTGAGAGGCTTTCACGTGAGAAAGAAACATAACTCACTTCTCCTA
TGTTGGCAAAGGACAGAACTCGTCGGAGTTTTCAGCATGGAGATGTCGCTCCTCCTGATTT
CCACCGGAGTTTCAATTATTAAAAAATATTTTCTTAATTCAATTTATCTTAAATGACA
AATTTTTAGTTTCTGATTTTATTTTGCTCAGTGCGATGGATTTTTAAATTTAAGTTTCAC
ACAAATATATAAATTTTTG

09265585-031099

FIG. 16E

SRPa6 (12398)

AATCGCTTGAACCGAATTTGGATCGAGATTCGAAAGAAAGGCTGAGAGTGGAGAGAGTGC
TGTTCCGTAGGAGGATTATGGATTTGGTCCGATCAGATGATGATAATAATAAACCGGGAA
CCCGGTTTGGGTTAATGGAGGAGAAAGAACAATGGAGAGTGTTGATGGAGAAAGCTGGAT
TTGAGCCGGTTAAACCGAGTAATTACGCGGTTAGCCAAGCGAAGCTGCTACTATGGAAC
ACAATTATAGTACATTGTATTCACTTGTTGAATCGGAGCCAGGTTTCATCTCCTTGGCTT
GGAACAATGTGCCTCTCCTCACCGTTTCCTCTTGGCGTTGACTACTTGGTCCGATAAGTT
AATCTAGTATTTTGAAGTTAGCTTTTGAATTGAATTGTTTGGGGTTAGATTTGGATGTTT
AATTAGTCTCTAGCCTATTCTCTTACTCTTTTTTGTCTAGTGCTTGGAGTGATGATGGTT
TGTCGTTTATGTTTCATTTGTAATATATATTGTATGTAACATTTGACTAAAAAAAAAAAA
AAAAAAA

09265585 "031099

FIG. 16F

SRPa7 (21729/3635/17410)

AAAGACTTTAGCAGATTTTCAAGCGGCTCAGAACATCAACAACAACAACAACAACCG
TTTTATAGTCAAGCAGCTCTCAACGCTTTTCTTTCAAGGTCTGTGAAGCCTCGAAATTAT
CAGAATTTTCAATCTCCGTCGGCCGATGATTGATCTCACGTCGGTGAATGATATGAGTTT
GTTTGGTGGTTCTGGTTCATCTCAGCGTTACGGTTTACCGGTTCCCAGGTCTCAGACGCA
ACAGCAACAATCGGATTACGGTTTATTTGGTGGGATCCGAATGGGAATCGGGTCGGGTAT
TAATAATTATCCAACATTAACCGGCGTTCCGTGTATTGAACCGGTTCAAAACCGGGTTCA
TGAATCGGAGAACATGTTGAATAGTTTAAGAGAGCTTGAGAAACAGCTTTTAGATGATGA
CGATGAGAGTGGTGGTGAATGATGACGTGTGAGTTATAACAAATTCAAATTCGATTGGAT
TCAAATCTCGTGACTCCGAACCCGAACCCGAACCCGGTTTGTCTTTTACCGAGCTC
TTCTTCTTCGTCTTCTTCGCCTTCTACAGCTTCGACGACGACATCGGTATGTTCTAGGCA
AACGGTTATGGAAATCGCGACGGCGATCGCGGAAGGAAAAACAGAGATAGCGACGGAGAT
TTTGGCGCGTGTCTTCTCAAACGCCTAATCTTGAGAGGAATTCAGAGGAGAAGCTTGTGA
TTTCATGGTGGCTGCGCTTCGATCGAGGATAGCTTCTCCAGTGACGGAATTGTATGGGAA
GGAGCATTTAATCTCGACTCAATTGCTCTACGAGCTCTCTCCTTGTTCAAACTCGGTTT
CGAGGCCGCGAATCTCGCCATTCTCGACGCCGCCGATAACAACGACGGTGGGAATGATGAT
ACCGCACGTTATCGATTTTCGATATCGGAGAAGGTGGACAATACGTTAACCTTCTCCGTAC
ATTATCCACGCGCCGGAATGGTAAAAGTCAGAGTCAGAATTCTCCGGTGGTTAAGATCAC
CGCCGTGGCGAACAACGTTTACGGATGTTTAGTCGATGACGGTGGAGAAGAGAGGTTAAA
AGCCGTGGAGATTTGTTGAGCCAACTCGGTGATCGACTCGGTATCTCCGTAAGTTTCAA
CGTGGTGACGAGTTTACGACTCGGTGATCTGAATCGTGAATCTCTCGGGTGTGATCCCGA
CGAGACTTTGGCTGTGAACCTTAGCTTTCAAGCTTTATCGTGTTCCCGACGAAAGCGTATG
CACGGAGAATCCAAGAGACGAACCTTCTCCGGCGCGTGAAGGGACTTAAACCGCGCGTGGT
TACTCTAGTGGAGCAAGAAATGAATTGGAATACGGCGCCGTTTTTAGGGAGAGTGAGTGA
GTCATGCGCGTGTACGGTGCGTTGCTTGAGTCGGTCGAGTCTACGGTTCCTAGTACGAA
TTCCGACCGTGCCAAAGTTGAGGAAGGAATTGGCCGGAAGCTAGTAAACGCGGTGGCGTG
CGAAGGAATCGATCGTATAGAGCGGTGCGAGGTGTTTCGGGAAATGGCGAATGCGGATGAG
CATGGCTGGGTTTGAAGTTAATGCCATTGAGTGAGAAGATAGCGGAGTCGATGAAGAGTCG
TGGAACCGAGTCCACCCGGGCTTTACCGTTAAAGAAGATAACGGAGGTGTGTGCTTTGG
TTGGATGGGACGGGCACTCACTGTGCGATCCGCTTGGCGTTAACTTCACACACTCTTTT
TTTCTTCTTATTATTACCATATTATTATTAATTTTCGAGATTATTCTGATATTATTATCA
TTGTGATTTTCCGTTTTCGAAAAGTGTAGGAATCTTATGTAAACAAAGAAAAAAAAAAGACT
TTTATGTTTTTCTAATAATAAAGAAAGAGTGATTGGGTTCAAAAAAAAAAAAAAAAAA
AAAAAAA

09265585.031099

FIG. 16G

SRPa8 (10964)

TGCATACAACGCACCGTTTTTCGTAACACGGTTTTCGCGAAGCTCTATTTTCATTTCTCCTC
GATTTTTGACATGCTTGAGACAATTGTGCCACGAGAAGACGAAGAGAGGATGTTCTTGA
GATGGAGGTCTTTGGGAGAGAGGCACTGAATGTGATTGCTTGCGAAGGTTGGGAAAGAGT
GGAGAGGCCTGAGACATACAAGCAGTGGCACGTACGGGGCTATGAGGTCAGGGTTGGTGCA
GGTTCCATTTGACCCAAGCATTATGAAGACATCGCTGCATAAGGTCCACACATTCTACCA
CAAGGATTTTGTGATCGATCAAGATAACCGGTGGCTCTTGCAAGGCTGGAAGGGAAGAAC
TGTCATGGCTCTTTCTGTTTGGAAACCAGAGTCCAAGGCTTGACCGAGAAATCCTCGTTG
GCATATGAGAGACCATCTCTTGATTTTCTTCCTGTGTAATTCAGAGACAGAATTACAG
ATGTAAGAAGAGAATGCTGCACAAAGAACTTGTTCAAAGATAATATTGATGTAAGTCCTG
TTTTATAACTTTCTAGCTGTGTTTTGTTGTTTCTCAGCTAGATTCTCCTAACGGTATTC
TTGTAGCTAGGGTGATCAGATTGTTTGTATATTGCTAGCAGAGTTAGTTTGTCTAGATTG
TAACACATATAAGAGGAAGCTTAGAGTTTCTATGGTTTAAAGAGAAGTTTTTTCCTTCTC
CAATGTAAAAAAAAAAAAAAAAAAAA

09265585.031099

FIG. 16H

SRPa10 (11261)

AAAAAATGGGAAACCATCACTCTTGATGAACTTATGATCAATCCAGGAGAGACAACGGTC
GTCAACTGCATTTCATCGGTTACAATACACTCCTGATGAAACTGTGTCATTAGACTCTCCA
AGAGACACGGTTCTGAAGCTATTCAGAGATATCAATCCTGACCTCTTTGTGTTTGCAGAG
ATTAACGGAATGTACAACTCTCCTTTCTTCATGACGAGGTTCCGAGAAGCGCTTTTTCAT
TACTCTTCACTCTTTGACATGTTTGACACCACAATACACGCAGAGGATGAGTACAAAAAC
AGGTCACCTGTTGGAGAGAGAGTACTTGTGAGAGACGCGATGAGCGTGATTTCCTGCGAG
GGTGCAGAGCGGTTTGCGAGGCCTGAAACCTACAAGCAATGGCGAGTTAGGATTTTGAGA
GCCGGGTTTAAGCCAGCAACTATTAGCAAAACAGATCATGAAGGAGGCTAAGGAAATTGTG
AGGAAACGTTACCATAGAGATTTTGTGATCGATAGCGATAACAATTGGATGCTTCAAGGA
TGGAAGGAAGAGTCATCTATGCTTTTTCTTGCTGGAAACCTGCTGAGAAGTTCACAAAC
AATAATTTAAACATCTGAAAAATGTTACTTCTCAATTACATCATTTTTGTGTTCCCAATGG
TTTTGTAGAATATGTTTGATCCCGTGAGTGGATGCAACTCTTTTTTCCTGCAAGTACATA
TTGTATTCAAATCCTTGTGGAAATGATAAATTGTTTAATCAAAAAAAAAAAAAA

09265585 "031099

FIG. 16I

SRPa11 (18652)

GCGAATGTTGAGATCTTGGAAGCAATAGCTGGGGAAACCAGAGTCCACATTATCGATTTT
CAGATTGCACAGGGATCACAATACATGTTTTTTGATTTCAGGAGCTTGCGAAACGCCCTGGT
GGGCCGCCGTTGCTGCGTGTGACGGGTGTGGATGATTCACAGTCCACCTATGCTCGTGGG
GGAGGACTCAGCTTGGTAGGTGAGAGGCTTGCAACTTTGGCGCAGTCATGTGGTGTCCCG
TTTGAGTTTCACGATGCCATCATGTCTGGGTGCAAGGTGCAGCGGGAACATCTCGGGTTG
GAACCTGGCTTTGCTGTTGTTGTGAACTTCCCATATGTATTACACCACATGCCAGACGAG
AGCGTAAGTGTGAAAAATACAGAGACAGGCTGCTGCATCTGATCAAGAGCCTCTCCCA
AACTGGTTACTCTAGTAGAGCAAGAATCCAACACAAACACCTCGCCATTGGTGTACGG
TTTGTGGAAACACTGGATTACTACACAGCGATGTTTGAGTCGATAGATGCAGCACGGCCA
CGGGATGATAAGCAGAGAATCAGCGCAGAACAACTGTGTAGCAAGAGACATAGTGAAC
ATGATAGCATGTGAGGAGTCAGAGAGAGTAGAGAGACACGAGGTACTGGGGAAATGGAGG
GTCAGAATGATGATGGCTGGGTTACGGGTGGCCGGTCAGCACATCTGCAGCGTTTGCA
GCGAGTGAGATGCTGAAAGCTTATGACAAAACTACAACTGGGAGGCCATGAAGGAGCG
CTCTACCTCTTCTGGAAGAGACGACCCATGGCTACATGTTCCGTGTGGAAGCCAAACCA
AACTATATTGGGTAAGTTATAGTGATGATGGTTACTTGAGTGGATAAAGAAGAGCACAA
AAAAACACATCTGTCGCTGTAAATTTTTTAGGATGTGCAATGATGTTTTAAGTTGTAACA
CAACCTAAGTTATATATGTATACAAACCAACCTGGTGGTTGTTTTCTCTTGTAATTG
TCATGTGGTTGTGGGTGGGAAGCTAGTAATGAAATATAACCAAAACATTGATTAGGTCAA
AAAAAAAAAAAA

660150 5855250

FIG. 16J

SRPa12 (23196) *

TCTTACTCAAGGTTCTTCTTTGTCATCTTGTGCGGAATCCACAAAGAGGAGAATAAAGA
TTCGACCTTTATTAGATATTAACGACTCTGGATTTTGGGTTTTGGAGTTGGATCCACA
TGGGTTCTTATCCGGATGGATTCCCTGGATCCATGGACGAGTTGGATTTCAATAAGGACT
TTGATTTGCCTCCCTCCTCAAACCAAACCTTAGGTTTAGCTAATGGGTTCTATTTAGATG
ACTTAGATTTCTCATCCTTGGATCCTCCAGAGGCATATCCCTCCCAGAACAACAACA
ACAACATCAACAACAAGCTGTAGCAGGAGATCTGTTATCATCTTCATCTGATGACGCTG
ATTTCTCTGATTCTGTTTTGAAGTATATAAGCCAAGTTCTTATGGAAGAGGATATGGAAG
AGAAGCCTTGTATGTTTCATGATGCTTTGGCTCTTCAAGCTGCTGAGAAATCTCTCTATG
AGGCTCTTGGTGAGAAAGACCCTTCTTCGTCTTCTGCTTCTTCTGTGGATCATCCTGAGA
GATTGGCTAGTCATAGCCCTGACGGTTCTTGTTCAGGTGGTGCTTTTAGTGATTACGCTA
GCACCACTACCACTACTTCTCTGATTCTCACTGGAGTGTGATGGTTTGGAGAATAGAC
CTTCTTGGTTACATACACCTATGCCGAGTAATTTTGTTTTCCAGTCTACTTCTAGGTCCA
ACAGTGTCAACCGGTGGTGGTGGTGGTGGTAAATAGTGCGGTTTACGGTTCAGGTTTTGGCG
ATGATTTGGTTTCGAATATGTTTAAAGATGATGAATTGGCTATGCAGTTCAAGAAAGGGG
TTGAGGAAGCTAGTAAGTTCCTTCCTAAGTCTTCTCAGCTCTTTATTGATGTGGATAGTT
ACATCCCTATGAATTCTGGTTCCAAGGAAAATGGTTCTGAGGTTTTTGTAAAGACGGAGA
AGAAAGATGAGACAGAGCATCATCATCATATGATGCACCACCACCAACAGATTAA
CTGGTAAGAAAAGCCATTGGCGCGACGAAGATGAAGATTTGTTGAAGAAAGAAGTAACA
AGCAATCAGCTGTTTATGTTGAGGAAAGCGAGCTTTCTGAAATGTTTGATAACATGTTCC
TATGTGGCCCTGGGAAACCTGTATGCATTCTTAACCAGAACTTTCCTACAGAATCCGCTA
AAGTCGTGACCGCACAGTCAAATGGAGCAAAGATTCGTGGGAAGAAATCAACTTCTACTA
GTCATAGTAACGATTCTAAGAAAGAACTGCTGATTTGAGGACTCTTTTGGTGTATGTG
CACAAGCTGTATCAGTGGATGATCGTAGAACCGCCAACGTTTAGCTAAGGCAGATACGAG
AGCATTCTTCGCCTCTAGGCAATGGTTCAGAGCGGTTGGCTCATTATTTTGCAAATAGTC
TTGAAGCACGCTTAGCTGGGACCGGTACACAGATCTACACCGCTTTATCTTCGAAGAAAA
CGTCTGCAGCAGACATGTTGAAGGCTTACCAGACATACATGTCCGTCTGCCCTTTCAAGA
AAGCTGCTATCATATTTGCTAACCACAGCATGATGCGTTTCACTGCAAACGCCAACACGA
TCCACATAATAGATTTTCGGAATATCTTACGGTTTTTCACTGGCCTGCTCTGATTCATCGCC
TCTCGCTCAGCAGACCTGGTGGTTCGCCTAAGCTTCGAATTACCGGTNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNGAGTTCAGGAGACAGGTCATCGCTTGGCTCGATACT
GTCAGCGACACAATGTTCCGTTTGAGTACAACGCAATTGCTCAGAAATGGGGAAACGATC
CAAGTCGAAGACTTAAAGCTTCGACAAGGAGAGTATGTGGTTGTGAACCTTTGTTCGGT
TTCAGGAACCTTCTAGATGAGACCGTTCTGGTAAACAGCCCGAGAGATGCAGTTTTGAAG
CTGATAAGAAAAATAAACCCGAATGTCCTTCATTCCAGCGATCTTAAGCGGGAATTACAAC
GCGCCATTCTTTGTACGAGGTTTCAGAGAAGCGTTGTTTCATTACTCGGCTGTGTTTGAT
ATGTGTGACTCGAAGCTAGCTAGGGAAGACGAGATGAGGCTGATGTATGTGTTGAGTTT
TATGGGAGAGAGATTGTGAATGTTGTGGCTTCTGAAGGAACAGAGAGAGTGGAGAGCCGA
GAGACATATAAGCAGTGGCAGGCGAGACTGATCCGAGCCGGATTTAGACAGCTTCGCTT
GAGAAGGAACTGATGCAGAATCTGAAGTTGAAAATCGAAAACGGGTACGATAAAAACTTC
GATGTTGATCAAAACGGTAACTGGTTACTTCAAGGGTGGAAAGGTAGAATCGTGTATGCT
TCATCTCTATGGGTTCTTTCGTCTTCATAGATGTTGTTTCTTACGTTCTAAGCGACTGGG
ATTTATGTAGGGCTTTTCTGTTGATAGTCTCTCGCCAACACGAGTGGATTAAGTTCAGAG
TTAGGGTTCTTGAACACTAGAATGTTGTTATATTATGCTTGTGACATAGCGTGTGTAAGA
GTGTAGCCTAAGAGATATAGTACTCATTGCATGATCTTTTGCTATATGTTNCATGT

FIG. 16K

SRPd1

TCTGCAGACAATTTTNAGGAGGCCAATACCATGCTATTGGAAATTCAGAACTG
TCCACACCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTACTTCTCAGAGGN
AATGTCGGNNAGATTAGCTCCTGCTTAGGAATCTATGCTTCTCTCCNGC
AACAGTGGTGCCTCCTCATGGTCAGAAAGTGGCCTCA

04261555-031059

FIG. 16L

SRPg1

TCAACTGAGAATCTAGAAGATGCCAACAAGATGCTTCTGGAGATTTCTCAGTTA
TCAACACCGTTCNNCACTTCAGCACAGCGTGTGGCAGCATATTTCTCAGAAGCC
ATATCAGCAAGGTTGGTGAGTTCATGTCTAGGGATATACGCAACTTTGCCACAC
ACACACCAAAGCCACAAGGTAGCTTCAGCTTTTCAAGTGTTCAATGGTATTAGT
CCTTTAGTGGAGTTCTCACACTTCACAGCAAACCAAGCAATTCAAGAAGCCTTC
GAAAGAGAAGAGAGGGTGACATCATAGATCTTGATATAATGCAAGGGTTG

09265585, 031099

FIG. 16M

SRPp1

TCTGCAGACAACTTTGAAGAAGCCAATACAATACTGCCTCAGATCACAGAACTC
TCCACCCCCTATNGCAACTCGGTGCAACGAGTGGCTGCCTATNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNTGCATAGGAATGTATTCTCCTCTCCCTCCT
ATTACATGTCCCAGAGCCAGAAAATTGTGAAT

0925585.031099

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100

GATATCAGCATCATCAATTAATGTAAGTTGGCAAAGATCATGAGGGTTCTCATAGT
AATTTGGCCACAAGTATGACATCTGTCTCAATTGAGCAATCTAGTAGAGAACTGATCCA
TCATATATTGCTCATATTGAAAGTGAAAAAGATATGCTCAAGAACCTAGTAGAGAAGCTA
AAAATTGAAAAATCTAGCTCTACTAGAAAAATATGATAGGTTGCCTGTTTCTCATGAAAA
TTTATTAGATAATCATATCATGGCTAGATGTCGCTCATGAGGTTGTTCTTGCTAGTTTAG
ATTCCTGTGGGCATTTCATCTCTTTTAGATGCACTAACATGATAGGAAGTTTCTAATCTGG
TGCTTCACAATTCTGGTGATTTCATGCTTCCTTCATTGCAATTGATATTGATGCTTGATTCT
ATGCTTCAGTCACTTTGTGCGTTTAATTGGTATTGTATGTATCACTAGATTGTAGGGTGT
CTGCAACTAGTGTTTCACCATGTGGTTTTTTAGTATCATTCGTATTAGTTTCTAACTTTC
TATTGATATATTAAAGTGATAACTAGTTTTAGAAATATTCTCTTGTGCCATTAATGCTAC
AACTTGTTTTTTAGCGTGTACGTTAGCATTATAATATTTCTTATTATGAAAGCGGAAGAG
AAACGCGCCCAACCAGAGCATCCACGTCGTCTCATTTTACCTTCATCGTTGGATCATAGA
TGAGCGGTCCACGGTGAACTCCGTTTGCTTGCAAACCACGTCCTCTACGCGCTGTTAAG
TAGCTTCTAGAAACATCACGATGTGTCCCGTCCATTCTTTAGGAGGAGCCGGATCCGGC
GCCGAGTCGCCCAAGGTCCCGACCGCCGCGGCTCGGCCGCCGCCGCAAGGAGCGGAA
GGAGGTGCAGCGGCGGAAGCAGCGCGCAGCAGGAGGGCCCTCCACCTGCTGAGTGCAGCG
TGCTGCTGCAGTGC GCGGAGGCGCGTGAACGCGGACAACCTCGACGACGCGCACCAGACGC
TGCTGGAGATCGCGGAGCTGGCCACGCGCTTCGGCACCTCGACCCAGCGCGTGGCCGCT
ACTTCGCGGAGGGCCATGTCGGCGCGCGTCTCGTCACTCTCCTGCTAGGCCTGTACGCGCGC
TGCCGCGGGCTCCCCGCGCGCGCGCTCCACGGCCGCGTGGCCGCGCGCTTCCAGG
TGTTCAACGGCATCAGCCCCCTTCGTCAAGTTCTCGCACTTCACCGCCAACCAGGCCATCC
AGGAGGCGTTCGAGCGGGAGGAGCGTGTGCACATCATCGACCTCGACATCATGCAGGGGC
TGCAGTGGCCGGGCTCTTCCACATCCTTGTCTCCCGCCCCGGCGGCCCGCCAGGGTCA
GGCTCACCGGCTGGGGGCGTCCATGGACGCGCTCGAGGCGACGGGGAAGCGCCTCTCCG
ACTTCGCCGACACGCTCGGCCTGCCCTTCGAGTTCTGCGCCGTGCGCGAGAAGGCCGGCA
ACGTTGACCCGCGAGAAGCTGGGCGTCACGCGGCGGGAGGCCGTGCGCGTCCACTGGCCGC
ACCACTCGCTTTACGACGTCATCGGCTCCGACTCCAACACGCTCTGGCTCATCCAAAGGT
CCTCCATTTTCTTCTCTGCTTTCTTCCATGTCAAATCTTGATGCAATCATGACCACTT
TTCAGCTGCTGACATTGGATAATGTGAGCTTTACGGCAAGCATCAAGTCGTGGTAGTACA
TCCATTACAGCTATTTCTAAATATTTCTTCGGAGGTTTCTGCTCATAGTAAAAAAAAT
CGCGTTTTGAAGCTCAAAGGCGATTTCTTCCGAGGTTTGCTGTTGAGCGCTATTTTGA
AACCCCATTTTCTCAATTGATTTTTATTTTTTAAAGAAAAATAGTTTATTTTTCTCTTG
TGAATGGAGTCCCAACTAACCTTATATATTAATAAAAAAACGCGTTTGGAGCTCAAACG
TCGTTTGTATGACCAACGACCTTATAGGTTTTAAAGGTTGAATCTTGACAATGCTTT
TGAAAGGTTGAATCTTGACAATGCTTTTGAAGATGATACTGTAGTGTAGTCTGTAGTGA
GCATCCTCCATGGTCTTTGGTGATCGAGAATTCTGCGAGCCCGGGGGATCC

FIG. 17B

Partial amino acid sequence of ZCARECROW protein

YQHHQFXMXVGKRSXGFSXXFGHKVXHCLNXAIXXRNXSIIYCSYKXKKRYAQEPSREAK
NXKIXLYXKNMIGCLFLMKIYXIIISWLDVAHEVVLASLDCGHSSLLDALTXXEVSNLV
LHNSGDSCFLHCNXYXCLIHASVTLCVXLVLYVSLDCRVSATSVSPCGFLVSFVLVSNFL
LIYXSDNXFXKYSLVPLMLQLVFSVYVSIIIFPYYESGRETRPTRASTSSHFTFIVGSXM
SGPRXTPFACKTTSSTRCXVASRNITMCPVHSFRRSRIRRRSRPRSRPPRPPPPRSGR
RCSGGSSATRRASTCXVLTLLLOCAEAVNADNLDDAHOTLLEIAELATPFGTSTORVAAY
FAEAMSARVVSSCLGLYAPLPPGSPAAARLHGRVAAAFQVFNGISPFFVKFSHFTANOAIQ
EAFEREERVHIIDLDIMOGLOWPGLFHILVSRPGGPPRVRLTGLGASMDALEATGKRLSD
FADTLGLPFEFCVAEAKAGNVDPQKLGVTREAVAVHWP HHSLYDVIGSDSNTLWLIORS
SIFLLCLSSMSNLDAIMTTFQLLTDNVSFTASIKSWXYIHYSYFXNILRRFPAHKKKS
RFEAQKAISSEVCCXALFWKPHFLNXFLFFKEKLVHFSLVKWSPKLTLLKKTREGAQNA
RCYDQPALXVXKGXILTMLLKRLNLDNAFEMILXC SLXWSILHGLWXSRI PAARGI

THE UNIVERSITY OF CHICAGO

350 396

SCR YAALPSRWMPQTH-SLKMVSAFQVFNGISPLVKFSHFTANQAIQEAFE

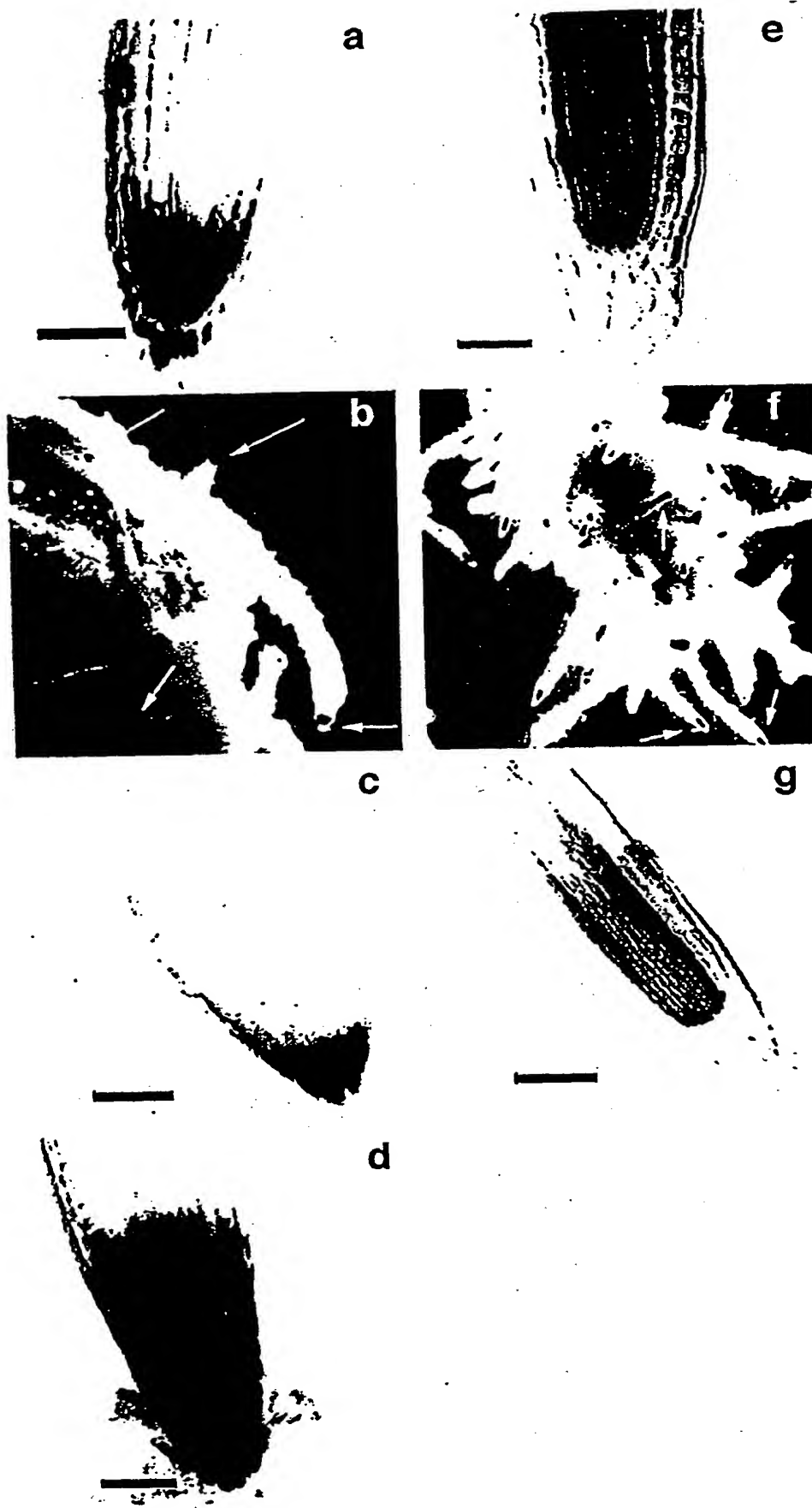
SRPd1 YASLPATVVP--PHGQKVAS

SRPg1 YATLP-----HTHQSHKVASAFQVFNGISPLVEFSHFTANQAIQEAFE

SRPp1 YSPLPPIxMSQ---SQKIVN

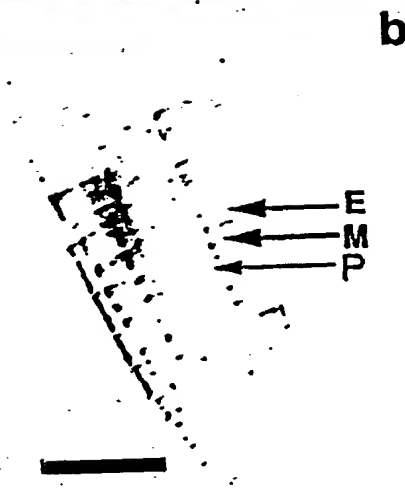
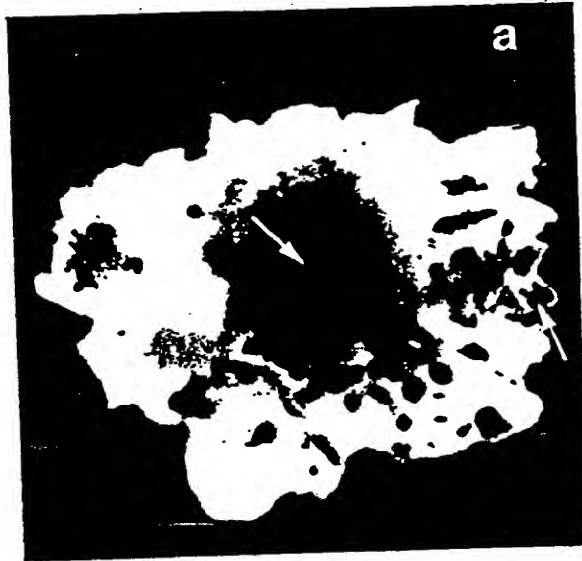
397 412
KEDSVHIIDLDIMQGL
REERVHIIDLDIMQGL

FIG. 19



09265585-031099

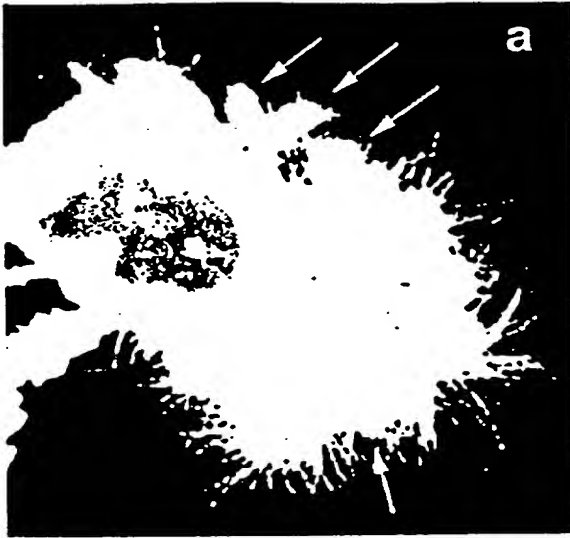
FIG. 20



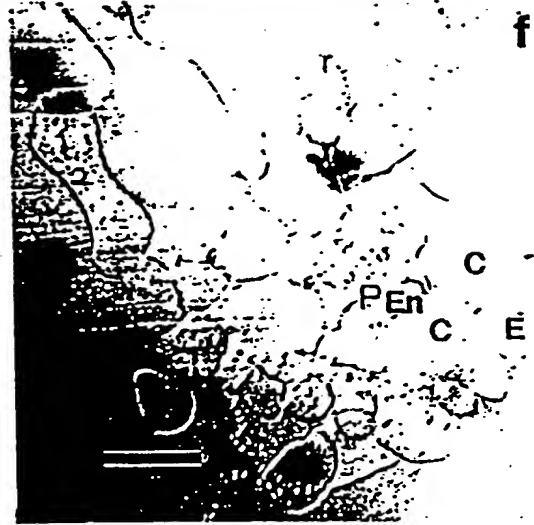
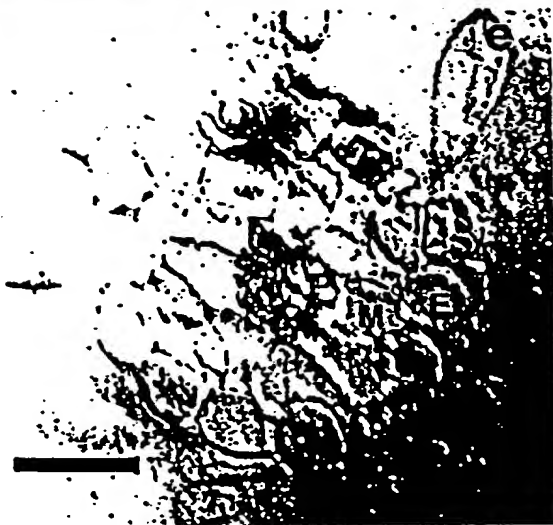
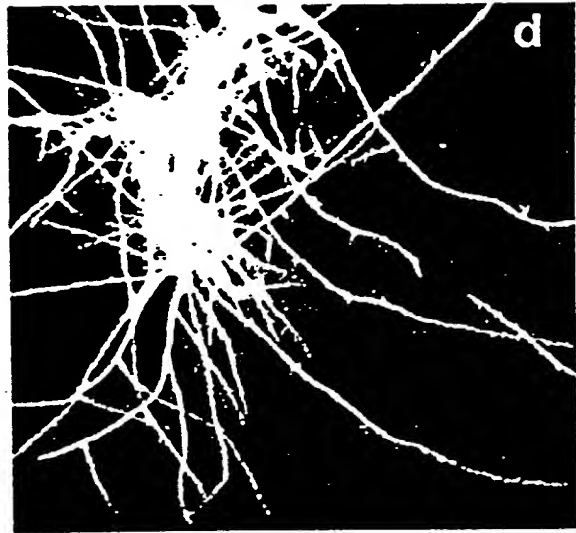
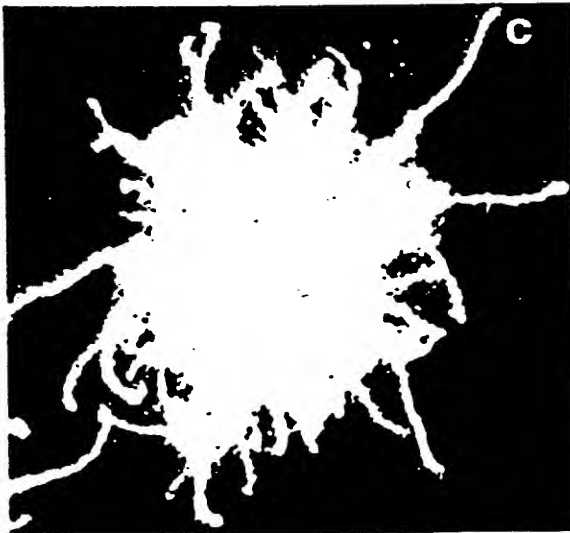
09265585-031099

FIG. 21

SCR Promoter::GUS



SCR Promoter::SCR



09265585-031099

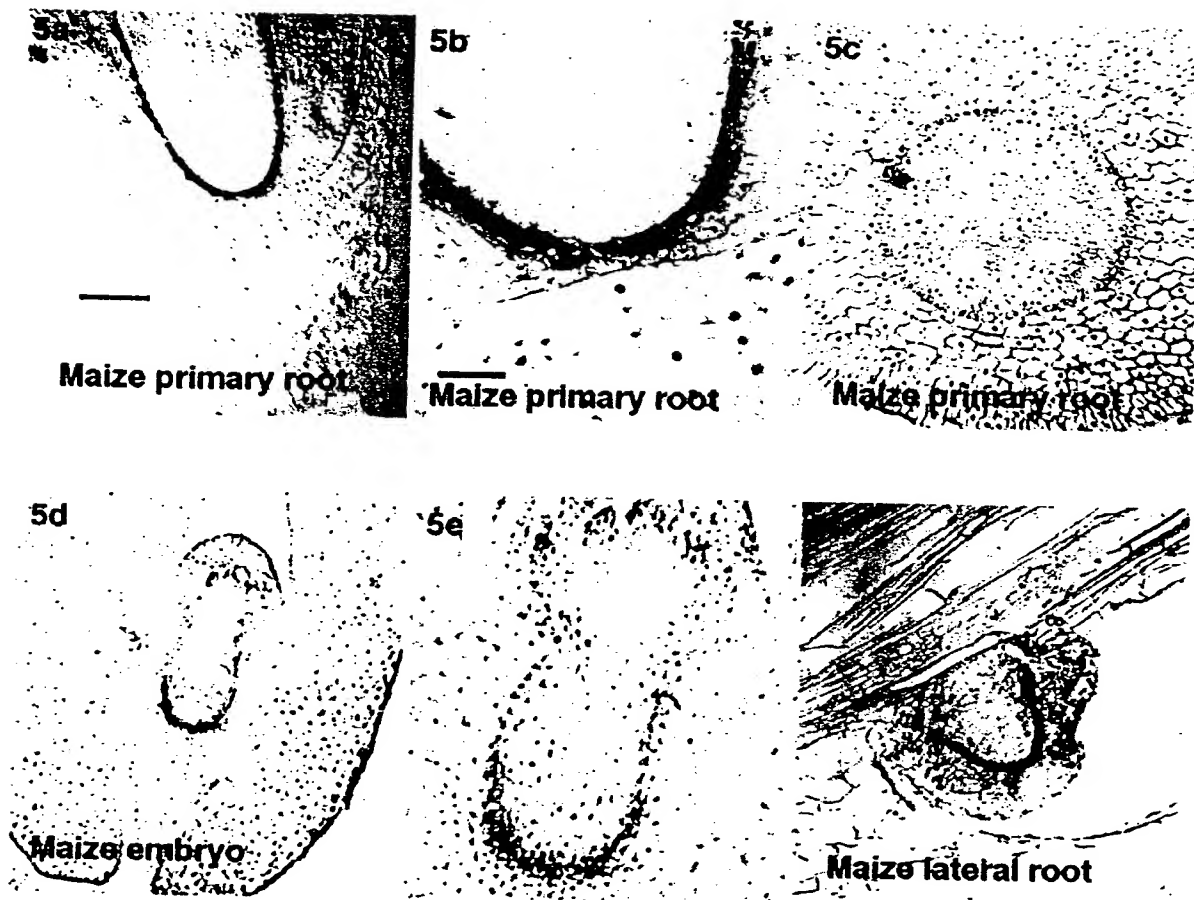
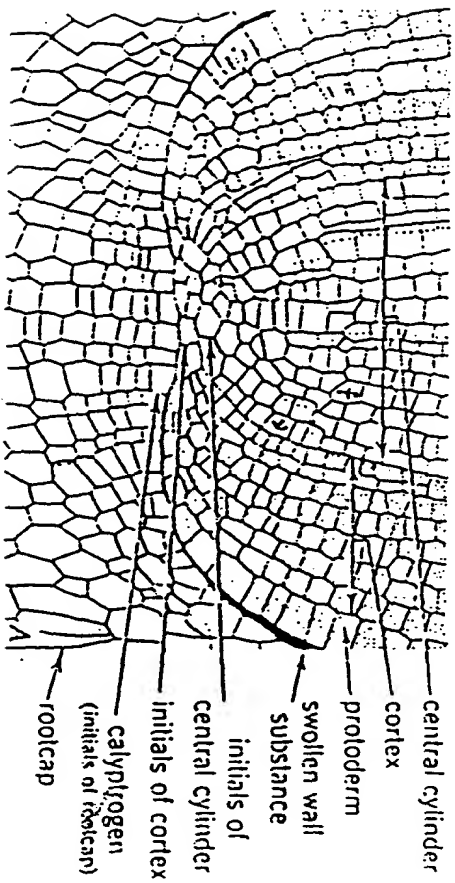
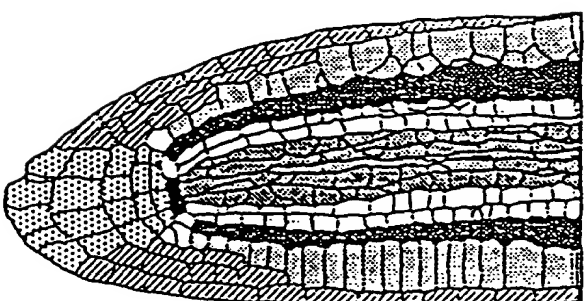


Fig. 22

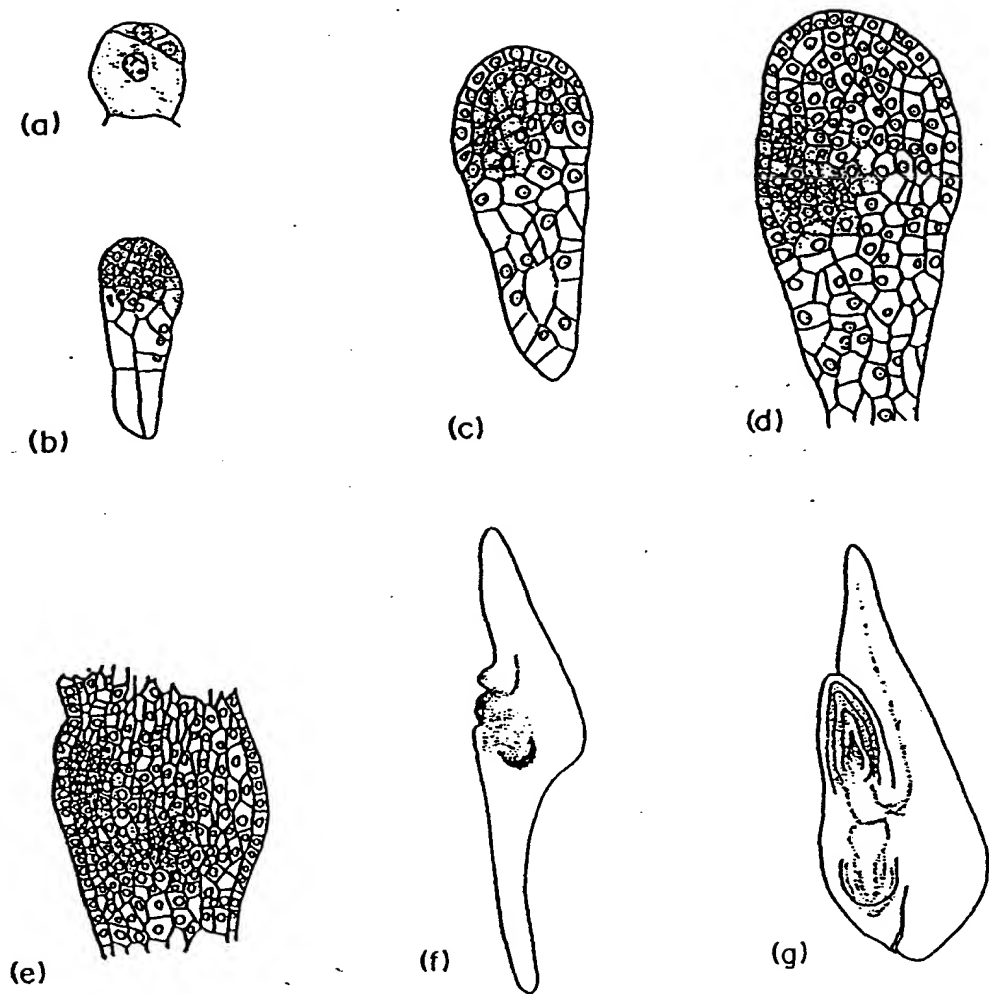


A. monocotyledonous closed-type (Zea).



B. dicotyledonous closed-type (Arabidopsis).

The schematic representation of the root apical meristems of maize (A.) And Arabidopsis (B.). Both show a type of a closed meristem in which all files of cells coverage onto a pole at the root apex, making the boundary between the root proper and the root cap discrete.



Embryo development in maize. (a) Three-celled embryo showing first division of terminal cell. (b)-(c) Embryos showing embryo proper and suspensor. (d)-(e) Embryos showing the initial development of shoot and root apical meristems. (f)-(g) Embryos showing the elaborate organization of shoot and root apical meristems.

ctgctagctcagcctactcactccactcaactcaccaccaactccactccgctcccgagc 60
 cgggactgactgactgactgtggtggtggtggtgcatcagcagcccgcgcgccgcaaaa 120
 cagcgaactgctccctccctcactcaccctatcccccgcgctgggtcgcccgatcgcc 180
 atgcgcgcggcggttctctcttggcggtttctagatgggctcctcctcctcctcctcttc 240
 tctctgctcctcctccgcgcgcatccaccgccccccactcctttccccactctcATGCCACC 300
 1 M P P
 GCCACCGCCTCCGCCTCCTCTCACTCCTTATTGCCGCGCTGCCCTCCCCACACCTCCC 360
 4 P P P P P P L T P Y C R R C P P P H L P
 TCCGCCTCCTCCTTCTTCCCCAAACCACTTCTCCTCCACTACCTCCATCAGCTAGACCA 420
 24 P P P P S S P N H F L L H Y L H Q L D H
 CCAAGAAGCCGCCGCCGCCCATGGTCCGCAAGCGCCCCGCGTCCGACATGGACCTCCC 480
 44 Q E A A A A A M V R K R P A S D M D L P
 GCCGCCGCGCCGCCACGTACGGGCGACCTCTCCGACGTACGGCGGCCGCTGCCGCCGG 540
 64 P P R R H V T G D L S D V T A A A A A G
 TGTGTTGGTAGTGGCGCGCCGTCTCCGCCAGCGCGCAGCTGCCCGCGCTGCCACCCA 600
 84 V G G S G A P S S A S A Q L P A L P T Q
 GCTCCACCAGCTGCCCGCCGCGTCCAGCACCACGCGCCGAGGTGGACGTGCCCGCGCA 660
 104 L H Q L P P A F Q H H A P E V D V P A H
 CCCGGCCCCGGCGCCGCCACGCGCAGGCGGGCGGCGAGGCAACCGCGTCCACGACCGCGTG 720
 124 P A P A A H A Q A G G E A T A S T T A W
 GGTGGACGGCATCATCCGCGACATCATCGGGAGCAGCGGCGGCGCGCGGTCTCCATCAC 780
 144 V D G I I R D I I G S S G G A A V S I T
 GCAGCTCATCCACAACGTCCGCGAGATCATCCACCCCTGCAACCCCGGCCCTCGCGTCGCT 840
 164 Q L I H N V R E I I H P C N P G L A S L
 CCTGGAGCTCCGCCTCCGCTCCCTCCTCGCAGCCGACCCGGCCCCACTGCCCGCCGCCGCC 900
 184 L E L R L R S L L A A D P A P L P P P P
 GCAGCCGACGAGCATGCTCTCCTGCACGGCGCTCCGGCCGCGCTCCCGCGGGCTGAC 960
 204 Q P Q Q H A L L H G A P A A A A P A G L T
 GCTCCCTCCCCCGCCACCGCTTCCGACAAGCGCCGCCACGAGCATCCACCGCGCTGCCA 1020
 224 L P P P P P L P D K R R H E H P P P C Q
 GCAGCAACAGCAGGAGGAACCGCATCCGGCGCCGACGTGCGCCAAGGCCCGACCGCGGA 1080
 244 Q Q Q Q E E P H P A P Q S P K A P T A E
 AGAGACCGCAGCGGCGGCCGCCGCCGACAAGCAGCAGCTGCTGCGGCCGCCAAGGAGCG 1140
 264 E T A A A A A A A Q A A A A A A A K E R
 GAAGGAGGAGCAGCGCGGAAGCAGCGCAGCAGGAGGGCCTCCACCTGCTGACGCTGCT 1200
 284 K E E Q R R K Q R D E E G L H L L T L L
 GCTGCACTGCGCCGAGGCCGTGAACGCGGACAACCTGGACGACGCGCACCAGACGCTGCT 1260
 304 L Q C A E A V N A D N L D D A H Q T L L
 GGAGATCGCGGAGCTAGCGACGCCGTTCCGGCACCTCGACGACGCGCGTGGCCGCCCTACTT 1320
 324 E I A E L A T P F G T S T Q R V A A Y F
 CGCGGAGGCCATGTGCGCGCGGCTCGTCAGCTCCTGCCTGGGCCTGTACGCGCCGCTGCC 1380
 344 A E A M S A R L V S S C L G L Y A P L P
 GCCGGGCTCCCCCGCGCGCGCGCCTCCACGGCCGCGTCCGCCGCCGCTTCCAGGTGTT 1440
 364 P G S P A A A R L H G R V A A A F Q V F
 CAACGGCATCAGCCCCCTTCGTCAAGTTCTCGCACTTACCCGCCAACCAGGCCATCCAGGA 1500
 384 N G I S P F V K F S H F T A N Q A I Q E
 GGCGTTCGAGCGGGAGGAGCGGTGCACATCATCGACCTCGACATCATGCAGGGGCTGCA 1560
 404 A F E R E R V H I I D L D I M Q G L Q
 GTGGCCGGGGCTCTTCCACATCCTTGCCTCCCGCCCCGGGGCCCCAGGGTGAGGCT 1620
 424 W P G L F H I L A S R P G G P P R V R L
 CACCGGCCCTCGGGGCGTCCATGGAGGCGCTCGAGGCCACGGGGAAGCGCTCTCCGATTT 1680
 444 T G L G A S M E A L E A T G K R L S D F
 CGCCGACACGCTCGGCCTGCCCTTCGAGTTCTGCGCCGTCGCCGAGAAGGCCGCAATGT 1740
 464 A D T L G L P F E F C A V A E K A G N V

Fig. 25A


```

TGACCCGGAGAAGCTAGGGGTCACGAGGCGGGAGGCCGTCGCCGTCCACTGGCTGCACCA 1800
484  D P E K L G V T R R E A V A V H W L H H
CTCGCTCTACGACGTCACCTGGCTCCGACTCCAACACGCTCTGGCTCATCCAAAAGtagga 1860
504  S L Y D V T G S D S N T L W L I Q R
aggagtacaccatctctcgatcctgacttccttgctaccatgtcaaactcttgatgcaatc 1920
atggccactttttcagctactaacacttttagtttagccaatgcgacatccagtacaactaa 1980
tctaaaaaaataatcttcagaggtttcctagtaaaaaaacgcggtttttggagctcaaaa 2040
agcttgatcattatgaccaaccaactttctaggcttaaaaagggttgaatcttggcaatgct 2100
tttgagacgatgctgtactgaagtactggtagagagagtatcctccatggcctttgttga 2160
tcccagaaccacaaaagatagtatcttcgctcgcatttggttagtgagggtgttctgatca 2220
tcacttgaggatggagctgaaagttcctatcatcatgaccaactttccatggcaaaagg 2280
tttctagttccaagtggcaggacgatgattactgagtactgaatggagtaactgtcatc 2340
ttctaccactaaccatcatttattaataacataaatcatcatccggagcctaaactcagaa 2400
aggctaatacaaaagtgaatctttctcaaatggctgccatagccagtggtagcatgcctg 2460
gccattgtactttttcgggtgaaccatctcgtctcaagcatgagatgaaggcctgaactgc 2520
aatgtccttgatttgatgcaaccattattagaagaaacgctaagcgatgccggtcctggc 2580
aagggaatgccatctcgtcagacagacagggattcgggaatcgaatggctagctggtgac 2640
aaatcgacggggattaataaaactacattgggtcattgattccatccccacacacctgca 2700
gGCTGGCCCCCAAGGTGGTGACAATGGTGGAGCAGGACCTGAGCCACTCGGGCTCCTTCC 2760
522  L A P K V V T M V E Q D L S H S G S F
TGGCGCGCTTCGTGGAGGCCATCCACTACTACTCGGCGCTGTTCTGACTCGCTGGACGCGA 2820
541  L A R F V E A I H Y Y S A L F D S L D A
GCTACGGCGAGGACAGCCCCGAGCGGCACGTCGTGGAGCAGCAGCTGCTGTCTCGCGGAGA 2880
561  S Y G E D S P E R H V V E Q Q L L S R E
TCCGCAACGTGCTGGCCGTGGGCGGGCCGCGCCGACCGGCGACGTCAAGTTCGGCAGCT 2940
581  I R N V L A V G G P A R T G D V K F G S
GGCGCGAGAAGCTGGCGCAGTCCGGGTTCGCGCGCCGCTCGCTCGCCGGCAGCGCCGCGG 3000
601  W R E K L A Q S G F R A A S L A G S A A
CGCAGGCGTCCCTGCTGCTCGGCATGTTCCCCCTCCGACGGGTACACGCTGGTGGAGGAGA 3060
621  A Q A S L L L G M F P S D G Y T L V E E
ACGGCGCGCTGAAGCTCGGGTGGAAGGACCTCTGCCTGCTCACCGCGTCCGCCCTGGCGCC 3120
641  N G A L K L G W K D L C L L T A S A W R
CCATCCAGGTGCCGCGCTGCCGTGATgagacctctgctgctcctgcttgcgttgagag 3180
661  P I Q V P P C R *
gccgccactccacttggttttgcattctgtagctgctcggttttggtcatcagctgggagata 3240
agaaaagcggaacgtactaattgctctggagtagatccatccattcacagtgatagtta 3300
ctgatgtactaagctttaattagttcaatgctagatcggttcttggttcaggtgtcgatcgc 3360
gtatccttgctccttggtctccttttcattttggtgctttgtctagtcgctttcccgacta 3420
atgccgtgctcttcatgcgcgttctagtgaagattcttgccgagaatattagcatagttt 3480
tcatgtaaagtagccatcaagcaagtatta 3510

```

Nucleotide and deduced amino acid sequence of the maize *SCARECROW*. Amino acid numbers are shown to the left; nucleotides are numbered on the right. Forward and reverse primers tested are underlined (J1050F and J1450R).

Fig. 25B

			*** *	**			
Zm	SCR	MPPPPPPPPPL	TPYCRRCPPP	HLPPPPSSP	NHFLHLYLHQ	LDHQEAAAAA	50
At	SCR	MAES-----	GDFNGGQPPP	HSPLRTTSSG	SSSSNN--RG	PPPPPPPPPLV	42
		***** ** *	*	*	*	** ** *	
Zm	SCR	MVRKRPAIDM	DLPP--PRR	HVTGDLSDVT	AAAAAGVGS	GAPS-SASAQ	96
At	SCR	MVRKRLASEM	SSNPDYNNSS	RPPRRVSHLL	DSNYNTVTFQ	QPPSLTAAAT	92
		*			*	** ** *	
Zm	SCR	LPALPTQLHQ	LP--PAFQHH	APEVDVPAHP	APAAH-AQAG	GEATASTTAW	143
At	SCR	VSSQPNPPLS	VCGFSGPLPVF	PSDRGGRNVM	MSVQPMQDQS	SSSSASPTVW	142
		** ** ** *	** ** *	** ** ** *	***** *	** *****	
Zm	SCR	VDGIIRDIIG	SSGGAAVSIT	QLIHNVREII	HPCNPGLASL	<u>LELRRLRSLLA</u>	193
At	SCR	VDAIIRDLIH	SS--TSVSIP	QLIQNVRDII	FPCNPNGAL	<u>LEYRLRSML</u>	190
		** *	* ** *		*	** ** *	
Zm	SCR	ADPAPLEPPP	QPQOHALLHG	APAAAPAGLT	LPPPPPLPDK	RRHEHPPPCQ	243
At	SCR	LDPSS-SSDP	SPQTFEPLYQ	ISNNPSP---	-PQQQQQHQQ	QQQQHKPPPP	235
		** *	* ** *	* ** *	* ** ** *	***** *	
Zm	SCR	QQQQEHPHPA	PQSPKAPTAE	ETAAAAAAQ	AAAAAAAKER	KEEQRRKQRD	293
At	SCR	PIQQQERENS	STDA-PQPE	TVTATVPAVQ	TNTAEALRER	KEEIKRQKQD	284
		***** ** *	***** ** *	** * ** *	** * ** *	** *****	
Zm	SCR	<u>EEGLHLLTLL</u>	LQCAEAVNAD	NLDDAHQTL	EIAELATPG	TSTQVAAAYF	343
At	SCR	<u>EEGLHLLTLL</u>	LQCAEAVSAD	NLEEANKLLL	EISQLSTPYG	TSAQVAAAYF	334
		*****	**** ** *		*****	***** ** *	
Zm	SCR	AEAMSARLVS	SLGLYAPLP	PGSPAAARLH	GRVAAAFQVF	NGISPFVKFS	393
At	SCR	SEAMSARLLN	SLGLIYAALP	SRWMPQTH-S	LKMVSFAQVF	NGISPLVKFS	383
		***** ** *	*** * ** *	***** ** *	***** ** *	***** ** *	
Zm	SCR	HFTANQAIQE	AFEREERVHI	IDLDIMQGLQ	WPGLFHILAS	RPGGPPRVRL	443
At	SCR	HFTANQAIQE	AFEKEDSVHI	IDLDIMQGLQ	WPGLFHILAS	RPGGPPHVRL	433
		**** ** *	***** ** *	* ***** *	**** ** *	* ** * *	
Zm	SCR	TGLGASMEAL	EATGKRLSDF	ADTLGLPFEF	CAVAEKAGNV	DPEKLGVTTR	493
At	SCR	TGLGTSMEAL	QATGKRLSDF	TDKLGLPFEF	CPLAEKVGNL	DERLNLVRKR	483
		***** *	***** ** *	**** ** *	***** ** *	*** ** *	
Zm	SCR	EAVAVHWLHH	SLYDVTGSDS	NTLWLIQRLA	PKVVTMVEQD	LSHSGSFLAR	543
At	SCR	EAVAVHWLQH	SLYDVTGSDA	HTLWLLQRLA	PKVVTVVEQD	LSHAGSFLGR	533
		***** ** *	***** ** *	* ***** *	***** ** *	***** *	
Zm	SCR	FVEAIHYISA	LFDSLDSYSG	EDSPERHVVE	QQLSREIRN	VLA VGGPART	593
At	SCR	FVEAIHYISA	LFDSLGSYSG	EESEERHVVE	QQLSKEIRN	VLA VGGPSRS	583
		* ** * ** *	* ** * ** *	**** ** *	***** ** *	***** ** *	
Zm	SCR	GDVKFGSWRE	KLAQSGFRAA	SLAGSAAAQA	SLLLGMPSPD	GYTLVEENGA	643
At	SCR	GEVKFESWRE	KMQQCQFGKI	SLAGNAATQA	TLLLGMPSPD	GYTLVDDNGT	633
		***** *	***** *				
Zm	SCR	LKLGWKDLCL	LTASAWRPIQ	VPPCR	668		
At	SCR	LKLGWKDLSL	LTASAWTPR-	----S	653		

Fig. 26A

09265585.031093

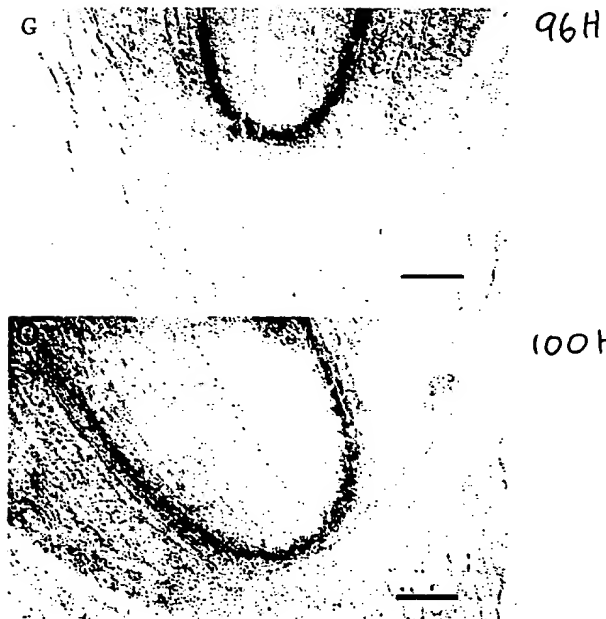
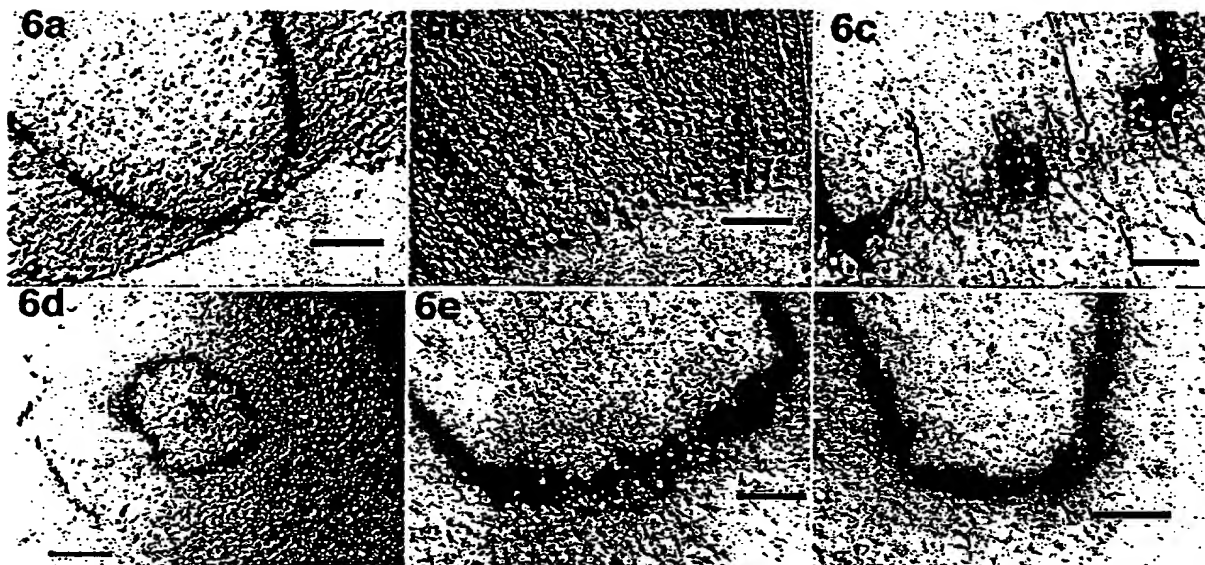


Fig. 27

06-03-2017

Fig. 28A

gagtacgatac ttaaagctat tcccggtgac gcgattctca atcagttcgc tatcgattcg
61 gcttcttcgt ctaaccaagg cggcggagga gatacgtata ctacaaacaa gcggttgaaa
121 tgetcaaacg gcgtcgtgga aaccactaca gcgacggctg agatcaactc ggcattgtgt
181 cctggttgac tcgcaggaga acggtgtgcg tctcgttcac gcgcttttgg cttgcgctga
241 aagctgttca gaaagagaat ctgactgtag cggantctgg tgaagcaaatt cggattctta
301 gccggtttctc aaatcgagac gatgagaaaa gtcgctactt act

Fig. 28B

Z34599

aaatttttca attacctaataaatgaaag ataagatctt aacaagtgac aaagggaaaa
61 acagtaggat ttagtttggc ttcggtcgga aatctatcat cataaccggt tcaacagatc
121 aattcattga gccaccatct aattggtgag agtttccaag ccgaggtggc tatgagcggc
181 cgtgtgtgcc aaccaacat gagacagccg tcaactctct ccacccgata accctcaccg
241 ccgttgaaca gagccaaaag cataactcgct tgcttaaacy cattcgaacc aatatgtgca
301 gccgcaaacc cagcagaccc gaaccggttc ctccantgac ttcaacgttt catgacgggt
361 caacttcggt ca

Fig. 28C

Z33772

ttttttttta agtgagaacc ttaacaaatt taaccatttg aactgaaata tgaacatgta
61 aagactcatt cacacttagc aaataggttt agaaccaaaa ctctaattat ttttatataa
121 tagggaaaaa aaagaaagaa aaattcttcc ataagtgtta gattagcttt tagtacctgt
181 gatcaccctt aacctctggt aataatacat ggagatgatt taaccagtta cacaataacc
241 caagattaca gtaaaaacat aattatgttt tatgaaacat aaagactata tgctcttgtc
301 acttatctta cctccaagct gaagcaacgg attaagcttt tctcctccca gcaaaaatgg
361 gagctcacc atttcttctt taaggttgta cttnttgca

Fig. 28D

Z37192

gctatggaag gagagaagat ggttcatgtg attgatctcg atgcttctga gccagctcaa
61 tggcttgctt tgcttcaagc ttttaactct aggctgaag gtccacctca tttgagaatc
121 actggtgttc atcaccagaa ggaagtgtt gaacaaatgg ctcatagact cattgaggaa
181 gcagagaaac tcgatatccc gtttcagttt aatcccgttg tgagtaggtt agactgttta
241 aatgtagnac agtttaggtt ttaaacagga gaggcnttag ccgtagctc ggttcttcaa
301 ttgcata

Fig. 28E

Z37191

ccgatcatca aattagttat cttcagctca aattggattt ggtttggtat tacaccaca
61 ccagaccaa ttgaaccaac acacaaaggc tttacatgca gaggcagtag aagcatttaa
121 gccaaaatag cataaagaga cagaaagtca ccatcacaaa acaactaaga ttgtgtcccc
181 atgtatacaa aaaagaaagg gactctgctc ataaccacaaa tagaagacaa actgtaatat
241 atcattcact tctgcatct ccaagctgat accgagtata gaggtcgatc ttgccagcaa
301 attactgcgc acccgntctc ttcttgatt ctatacccat caaaa

Fig. 28F

Z46550

gtggaattac aattacagca atttgatttc aattgttgaa tctaagcctg gttcatctc
61 tttggcctgg aacgatttac ctctctcac tctttcttcc tggcgataac caaaccaaac
121 cgatccggtg ttcttagttt tgttttggtt tcaatgttat ttttggttag acaaatattc
181 aattgttaat atactccgtg gtcagagtgt tttgttttcc ttttagttcg aacgttgaat
241 taattcaggg gtaggttttg aattctctga acctatgtg ttttttggtg acatcatttg
301 gatttgtgaa ctaggtttta aaactgggtc tagtcttggt gttttctcat tagataattt
361 aaactgggtt gtttctttat ttttggttg ggataaaagt gaccgg

Fig. 28G

Z38048

gtggaattnc aattacagca atttgatttc aattgttgaa tctaagcctg gttcatctc
61 tttggcctgg aacgatttac ctctctcac tctttcttcc angcgataac caaaccaaac
121 cgatgccggt attcttagtt ttgttttggt ttcaatgtta tttttggtta gacaaatatt
181 caattgttaa tatactccgt ggtcagagtg tttgttttn cttttagttc gaacgttgaa
241 ttaattcagg gtaggtttt gaattctctg aacctnatgt gttttntggt aacatcattt
301 ggatttgtga actaggttta aaaactggnc ttagtcttgt tgttttctca ttaggataat
361 ttaaactggt ttgcttcttt attttnggtt gggataaaagt gaccgg

Fig. 28H

Z38085

caaaactaca tttcatcact tttttgagca aaattacaaa taaaagagta gttacaaata
61 tatttggtt tcaacttct aattttatga aatagtaatt acatctcaaa cagatgacca
121 gaaccggtca ctttatccaa ccaaaaataa agaagcaaac cagttttaa tatctaata
181 gaaaacaaca agactaagac cagtttttaa acctagttca caaatccaaa tgatgttacc
241 aaaaaacaca taagggtcag agaattcaaa acctaccct ganttaattc aacgttcgaa
301 ctaaaagaaa aacaaaacac tctgaccacg gagtatatta acatttgatt atttgtctaa
361 ccaaaaataa cattgaaaac aaaacaaaac tanggaatac cggatcgg

Fig. 28I

F13896

cccaacgggt cctgagcttc ttacttatat gcatacttg tatgaagcct gcccttattt
61 caaattcgggt tatgaatctg ctaatggagc tatagctgaa gctgtgaaga acgaaagttt
121 tgtgcacatt atcgatttcc agattttctca aggtgggtcaa tgggtgagtt tgatccgtgc
181 tcttggtgct agacctgggtg gacctccgaa cgtaggata acgggaattg atgatccgag
241 atcatcgttt gctcgtcaag gaggacttgc agttagttgc acaaagcact tggca

Fig. 28J

F13897

gggtcatcaa catatcactt actactacaa catttgacaa cttgttcctn cggatcatgc
61 atgagtttta cttttacaaa cagattctgc aaactttaaa agcaagtttc taatctcttc
121 tgaaaccgaa caagggtttt attagttacc tccaagcaca agaagtgata agaggttgat
181 tcttccatcc taaatacaat gctccatctc tttcttcaag tgtatacttc tctgaataac
241 tctcaagcaa tcctttgatt gttgcgttca catacgagct caaaggatac ggtttaaadc
301 ccgccatgtg aaaccgaga

Fig. 28K

F13949

caaaaattta tatatttggtg tgaacttaaa tttaaaaatc catcgactg agcaaaataa
61 nntcagaaac taaaaatttg tcattttaaga taaattgaat taaggaaaat atttttttaa
121 taattgaaac tccggtggaa atcaggagga gcgacatctc catgctgaaa ctccgacgag
181 ttctgtcctt tgccaacata ggagaagtga gttatgtttc tcctcgacgt gaaagcctct
241 cactggcgtc cgttggnatna aacactcggc ttgagactcc gtgaagttac tgtgcgtcac
301 cggtgagaaa cccatctgta gaaacatcgc ttgccacgtc atcatcggcc tttctatcgg
361 acggctacga tccaacacca gcttctctat ctccggctgt ataaggaaa

Fig. 28L

T22782

ctatttttnac aattttatitt gttatttagaa gtggttagtgg agtgaaaaaa caaatcctaa
 61 gcagtcctaa ccgatccccg aagctaaaga ttctncacct tcccaaataa agcaaaacct
 121 agatccgaca ttgaaggaaa aaccttttag atccatctct gaaaaaaacc aaccatgaag
 181 agagatcatc atcatcatca tcatcaagat aagaagacta tgatgatgaa tgaagaagnc
 241 gacggtaacg gcatggatga gcttctagct gttcttggtt ataaggtag gtcatccgaa
 301 atggctgatg ttgctcaga aactcgagca gcttgaagtt atgatgtcta atgttcaagn
 361 aagncggtct ttntcaactt cgcnaactnn gactgttcac tntaatncgg cggngttttt
 421 caacgntggc ttgntttcna tgntnaccga ccttaat

Fig. 28M

T21627

atgggaaagg agcatttaat ctcgactcaa ttgctctacg agctctctcc ttgtttcaaa
 61 ctcggtttcg aggccgcgaa tctcgccatt ntcgacgccg ccgataacaa cgacggtgga
 121 atnatgatac cgcacgtaat cgatttcaat atcggagaag gtggacaata cgttaacctt
 181 ctccntacat tatccacgcg ccggaatggt aaaagtnaga gtcagaattc tccggtggtt
 241 aanatcaccg gccgtggcga acaacgttta cgggatgttt agtcggatga cgggtggnga
 301 agagaggttt aaaagcccgt ncgngntttt ttttgnagcc actncngntn atccg

Fig. 28N

H76979

actcggatc tccgtaagtt tcaacgtggt gacgagtta cgactcgggtg atctgaatcg
61 tnaatctntc ggggtgtnatc ccgacgagac tttggctgta aacttagctt tcaagcttta
121 tcgtgttccc gacgaaagcg tatncacgga gaatccaaga cgaacttctc cggcgcgtga
181 agggacttaa accgcgcgtg gttactctag tggagcaaga aatgaattcg aatacggcgc
241 cgttttttagg gagagtaagt nagtcatgcg cgtttnacgg tgcgttnctt gantcggtcg
301 agtctacggt tcctagtacg gatttccgac ccgtgccaaa atttnnggaa ggaatttgcc
361 cgnaannttn naaacgggt g

Fig. 280

N96767

atnaaaagtc tttttttttt ctttggtaca taagattcct acacttttcg aaatggaaaa
61 tcacaatgat aataatatca gaataatctc gaaaattaat aataatatgg taataataag
121 aagaaaaaaa aagagtgtgt gaagttaacg ccaagcggat gcgacagtga gtgcccgtcc
181 catccaacca aagcacacac ctccgttata ttctttaacg gttaaagccc ggtggactcg
241 gtttccacga ctcttcacg actccgctat cttctcactc aatggcatta actcaaacc
301 agccatgctc atccgcattc gccatttncc ggaacanctc gnaccgctct atacgntcga
361 ttccttcgga cggcaccgng ttttactagc ttccggncaa ttccttctn aactttggaa
421 cggtnggatt cgttcttggg accgtaggct tggcccgtt aagaacgnac cgtacagggg
481 nntgtttnt taatttcct taaaagggg cgnttttggg ttnatttttn ana

Fig. 28P

T43670

caaccntttt atagtcaagc agctctcaac gctttttttt caaggtctgt naagcctcga
 61 aattatcaga ntttncaatc tccgtcgccg atgattganc tcacgtcggt gaatgatatg
 121 agtttntttg gnggttcttg ttcattctcag cnttacgggt taccggttcc caggtctcan
 181 acgcaacagc aacaatcgga ttacggttta tttggtggga tccgaatggg aatcgggtcg
 241 ggtattaata attatccaac attaacgggc gttccgtgta ttgaaccggg tcaaaaccgg
 301 gttcatgaat cggaggacca ttgttganta agnttaagag agctttgtng aaacaanctt
 361 tttangattg atnaccg

Fig. 28Q

T76186

tgcatacaac gcaccgtttt tcgtaacacg gtttcgcaa gtctatttca tttctcctcg
 61 atttttgaca tgcttgagac aattgtgcca cgagaagacg aagagaggat gttccttgag
 121 atggaggtct ttgggagaga ggcactgaat gtaattgctt gcaagggttg ggaaagagtg
 181 gagaggcctg agacatacaa gcagtggcac gtacgggcta tgaggtcagg gttggtgcag
 241 gttccatttg acccaagcat tatgaagaca tcgctgcata aggtccacac attctaccac
 301 aaggattttg tgatcgggtca aagataaccg ggtggctctt tcaaggntgg aaggggaagg
 361 anctgtcatg ggtctttctt ttttgaaaac cagagtccca aggttttncc ggaaaatcct
 421 ccttggnnat tt nangnccc ttttttgtt ttttncccn gnnantccc nggggnagtt
 481 tccagtttna ggngngtttt tncnaaaa

Fig. 28R

T44774

tgcatacaac gcaccgtttt tngtaacacg gtttcgcgaa gtctatttna tttctcctcg
61 atttttgaca tgcttganac aattgtacca cgagaagacg aagagaggat gttccttgan
121 atggaggtct ttgggagana ggcactgaat gtaattnctt gcnaagggtg ggaaagagtg
181 gagaggcctg anacatacaa gcagtggcac gtacgggcta tgaggtcagg gttggtgcag
241 gttccatttg acccaagcat tatgaagaca tcgctgcata aggtccacac attctaccac
301 aagggttttt tgatccntcc aagataaccg gtggctcttn caaagctttg aaggggaagga
361 cttttcatgg gtcttttctt ttttggaacc aggtcccaag gttttncocg gaatccccgn
421 tggaattttg nnnccctttt tgattttttt tccccgnaa ttncoc

Fig. 28S

T45793

gagacggtag atccgncgcg ctaaagcttc ggcgaagtaa gtagccactt tnntnatagc
61 tccggcttga nacacagcta agcatccnat ttgcttcaca agagcttccg ctagagtcaa
121 attgtncnnc tggattgctt ctgcacaagc cataagcgcg tggactaaac gaacaccgtt
181 ctcttgcgag tnaaccagga taacagaacg anttgactca gccgcgcgcg tcgttgctgt
241 ggtggttgct gtcaccgtcg ttcttatgac tccaccaatn tgggtaccocg tcgaagtcga
301 tgtaaccata ggatcagggc ttcgngcatg nttttaaaac gg

Fig. 28T

T46205

gtttgattcg ttggaaggag ttccgaatag tcaagacaaa gtcattntctg aagtttactt
61 agggaaacag atttgtaatc nggtggcttg tnaagntcct gacagagtcg agagacacga
121 aacgttgagt caatngggaa accggtttgg ttcgtccggt ttagcgccgg cacatcttgg
181 gtctaacgcg ttaagcaag cnagtatnct tttntntgtn ttaaatagtg gccaaaggta
241 tctgtgtggag gagagtaatg gatgtttgat gttgggttgg cacactnngc ccactcattt
301 accacctccg gttttggaaa c

Fig. 28U

N96653

taaaaattga tcccaaaaag gcataaatta aaaatgacct accaaaacga tatatataag
61 aatttttaaac aagtgaacga aaataaataa aataaacaaa aggcaaaacg gttcgattca
121 gttcggttta ggtcttggtc cgaacatatg tcatcaccgg tccactgate tcaatctcaa
181 attcactcgn ctgcactcca ccaccgtcgt atgcttcgag tcaaactcag tacgnogccg
241 tcgagagttt ccaagcggag gtggtaatga gtggacgagt gtgccaaccc ancatcaaac
301 atccattact ttctccaca cgntaacctt ggccactatt taaacacagg caaaangcat
361 acttgtttgc ttaaaccgcg ttagnocnaa gntttgccgg gcgntaaacc cggcngaccc
421 aanccggntt tcccnatttg ctcaaacggt ttngtgnctt ttggcttttt gnatggcctt
481 taaangnncc

Fig. 28V

T76483

aaaaaatggg aaaccatcac tcttgatgaa cttatgatca atccaggaga gacaacggtc
61 gtcaacngca ttcacggtt acaatacacn cctgatgaaa ctgtgtcatt agactctcca
121 agagacacgg ttctgaagct attcagagat atcaatcctg acctctttgt gtttgcagag
181 attaacggaa tgtacaactc tcctttcttc atgacgaggt tccgagaagc gcttttncat
241 tacncttcac tctttgacat gtttgacacc acaatacacg gagaggatga gtacaaaaac
301 aggtcactgt ttggagagag agttactttt gaganacgcg nttgagcgtg attttctgc
361 nngggnttca nancgggtt tnnnggcctt aaaacctnca agaaatnggn ggtttgggtt
421 tt

Fig. 28W

F15454

aatcaatggt ttggttatat ttcattacta gcaaccacc cacaaccaca tgacaattta
61 caagagaaaa acaaccacca ggtttggtt gtatacatat ataacttagg ttgtgttaca
121 acttaaaaca tcattgcaca tcctaaaaat ttcagcgacc agaattgtgt tttgattgtg
181 cctctttctt tatccacctc aagtaacat cattcactat aacttaccca atct

Fig. 28X

N37425

gcgaatgttg agatcttgga agcaatagct ggggaaacca gagtccacat tatcgatttt
61 aagattgcac agggatcaca atacatgttt ttaattcagg agcttgcgaa acgccctggg
121 gggccgccgt tgctgcgtgt nacgggtgtg gatgattcan agtccaccta tgctcgtggg
181 ggaggactca gcttggtagg tgagaggctt gcaactttgg cgcagtcatg tgggtgtccc
241 ttttagtttc acgatgccat catgtctggg tgcaagggtc agcgggaaca tctcgggttg
301 gaacctggct ttgctgttgt tgtgaacttc ccatatgtat tacaccacat gccagacgag
361 agcgtaagtt ttgaaaatc acagngacag gcttctgcat ctnatcaana gcctttcccc
421 aaactggtac tctagtaggc aagattcaac acaacacttg catcna

Fig. 28Y

W43803

atgnaacata tagcaaaaga tcatgcaatg agtactatat ctcttaggct acactottac
61 acacgctatg tcacaagcat aatataacaa cattctagtg ttcaagaacc ctaactctga
121 acttaatcca ctctgtttgg cgagagacta tcaacagaaa agccctacat aaatcccagt
181 cgcttagaac gtaaganaca acatctatga agacgaagga acccatagag atgaagcata
241 cacgattcta cttttccacc cttgaagtaa ccagttaccg ttttgatcaa catcgaagtt
301 tttatcgtac ccgttttcgg attttcaact tcagattctg catcagttcc ttctcaagcg
361 gnagctgtcc taaatccggg tcgggtcagt ctcggtggc actgggtata tggctctggg
421 ctctccactc tctctggtct tcacaaggca cancattcac aatctntttt ccataaaaact
481 nnttttctn catnngncnn atnttggtt ccctnggntg gttgggggnc ncnt

Fig. 28Z

W43538

tcaaggttct tctttgtcat cttgttgccg aatccacaaa gaggagaata aagattcgac
61 ctttattaga tattaacgac tctggatttt tgggtttttg gagttggatc cacatgggtt
121 cttatccgga tggattccct ggatccatgg acgagttgga tttcaataag gactttgatt
181 tgcctccctc ctcaaaccac accttaggtt tagctaattg gttctattta gatgacttag
241 atttctcatc cttggatcct ccagaggcat atccctccca gaacaacanc aacaacatca
301 tcaacaacaa agctgtagca ggagatctgt tatcatcttc aactgaatga cgntggattc
361 tctgattctg ttttgagtat ataagccaag ttctnatggg agnnggtnat gnagagaagc
421 ctttgtatgt tcatgnngnt ttggnatta agntgctngg aaannactcn ntngnc

Fig. 28AA

SCL 1

LSMVNELRQI VSIQGDPSQR IAAYMVEGLA ARMAASGKFI YRALKCKEPP
SDERLAAMQV LFEVCPCFKF GFLAANGAIL EAIKGEEEVH IIDFDINQGN
QYMTLIRSIA ELPGKRPLR LTGIDDPESV QRSIGGLRII GLRLEQLAED
NGVSFKFKAM PSKTSIVSPS TLGCKPGETL IVNFAFQLHH MPDESVTTVN
QRDELLHMK SLNPKLVTVV EQDVNTNTSP FFPRFIEAYE YYSAVFESLD
MTLPRESQER MNVERQCLAR DIVNIVACEG EERIERYEAA GKWRARMMA
GFNPKPMSAK VTNNIQNLIK QQYCNKYKLK EEMGELHFCW EEKSLIVASA
WR*

Fig. 28AB

0925585-031099
65070"58559260

SCL 3

AMEGEKMHVH IDLDASEPAQ WLALLQAFNS RPEGPPHLRI TGVHHQKEVL
EQMAHRLIEE AEKLDIPFQF NPVVSRLDCL NVEQLRVKTG EALAVSSVLQ
LHTFLASDDD LMRKNCALRF HNNPSGVDLQ RVLMMSHGSA AEARENDMSN
NNGYSPSGDS ASSLPSPSSG RTDSFLNAIW GLSPKVMVVT EQSDHNGST
LMERLLESY TYAALFDCLE TKVPRTSQDR IKVEKMLFGE EIKNIISCEG
FERRERHEKL EKWSQRIDLA GFGNVPLSY AMLQARRLLQ GCGFDGYRIK
EESGCAVICW QDRPLYSVSA WRCRK*

Fig. 28AC

SCL 5

GTSPGTPELL TYMHILYEAC PYFKFGYESA NGAIAEAVKN ESFVHIIDFQ
ISQGGQWVSL IRALGARPGG PPNVRITGID DPRSSFARQG GLELVGQRLG
KLAEMCGVPF EFHGAALFCT EVEIEKLGVR NGEALAVNFP LVLHHMPDES
VTVENHRDRL LRLVKHLSPN VVTLVEQEAN TNTAPFLPRF VETMNHYLAV
FESIDVKLAR DHKERINVEQ HCLAREVENL IACEGVEREE RHEPLGKWRS
RFHMAGFKPY PLSSYVNATI KGLLESYSEK YTLLEERDGA YLGWKNQPLI
TSCAWR*

Fig. 28AD

09265585-031099

SCL 6

AAIFYGHHHH TPPPAKRLNP GPVGITEQLV KAAEVIESDT CLAQGILARL
NQQLSSPVGK PLERAAFYFK EALNNLLHNV SQTLPYSLI FKIAAYKSFS
EISPVLQFAN FTSNQALLES FHGFHRLHII DFDIGYGGQW ASLMQELVLR
DNAAPLSLKI TVFASPAHND QLELGFTQDN LKHFASEINI SLDIQVLSLD
LLGSISWPNS SEKEAVAVNI SAASFHSLPL VLRFBVKHLSL TIIVCSDRGC
ERTDLPFSQQ LAHSLHSHTA LFESLDAVNA NLDAMQKIER FLIQPEIEKL
VLDRSRPIER PMMTWQAMFL QMGFSPVTHS NFTESQAECL VQRTPVRGFH
VEKKHNSLLL CWQRTLVGV SAWRCRSS*

Fig. 28AE

SCL 11

KKWETITLDE LMINPGETTV VNCIHLQYT PDETIVSLDSP RDTVLKLFRD
INPDLFVFAE INGMYNPPFF MTRFREALFH YSSLFDMFDT TIHCERRDEV
ISCEGAERFA RPETYQWRV RILRAGFKPA TISKQIMKEA KEIVRKRYHR
DFVIDSDNNW MLQGWKGRVI YAFSCWKPAE KFTNNNLNI*

Fig. 28AF

0925585 031099
660750 5855260

SCL 13

ANVEILEAIA GETRVHIIDF QIAQGSQYMF LIQELAKRPG GPPLLRTVGV
DDSQSTYARG GGLSLVGERL ATLAQSCGVP FEFHDAIMSG CKVQREHLGL
EPGFAVVVNF PYVLHHMPDE SVSVEKYRDR LLHLIKSLSP KLVTLVEQES
NTNTSPLVSR FVETLDYYTA MFESIDAARP RDDKQRISAE QHCVARDIVN
MIACEESERV ERHEVLGKWR VRMMAGFTG WPVSTSAafa ASEMLKAYDK
NYKLGHEGA LYLFWKRRPM ATCSVWKPNP NYIG*

Fig. 28AG

SCL 14

LLKVLLCHLV AESTKRRIKI RPLLDINDSG FLGFWSWIHM GSYPDGFPGS
 MDELDFNKDF DLPPSSNQTL GLANGFYLDD LDFSSLDPPE AYPSQNNNNN
 NINNKA VAGD LLSSSSDDAD FSDSVLKYIS QVLMEEDMEE KPCMFHDALA
 LQAAEKSLYE ALGEKDPSSS SASSVDHPER LASHSPDGSC SGGAFSDYAS
 TTTTSSSDSH WSDGLENRP SWLHTPMPSN FVFQSTSRSN SVTGGGGGGN
 SAVYGSFGD DLVSNMFKDD ELAMQFKKGV EEASKFLPKS SQLFIDVDSY
 IPMNSGSKEN GSEVFKTEK KDETEHHHHH SYAPPPNRLT GKKSHWRDED
 EDFVEERSNK QSAVYVEESE LSEMFDNMFL CGPGKPCIL NQNFPTESAK
 VVTAQSNGAK IRGKKSTSTS HSNDKKETA DLRTLLVLCA QAVSVDDRRT
 ANVXLRQIRE HSSPLNGSE RLAHYFANSL EARLAGTGTQ IYTALSSKKT
 SAADMLKAYQ TYMSVCPFKK AAIIFANHSM MRFTANANTI HIIDFGISYG
 FQWPALIHRL SLSRPGGSPK LRITGIELPQ RGFRPAEEFR RQVIAWLDTV
 SDTMFRLSTT QLLRNGETIQ VEDLKLQGE YVVVNSLFRF RNLLDETVLV
 NSPRDAVLKL IRKINPNVFI PAILSGNYNA PFFVTRFREA LFHYSVDFDM
 CDSKLAREDE MRLMYVFEFY GREIVNVVAS EGTERVESRE TYKQWQARLI
 RAGFRQLPLE KELMQNLKLK IENGYDKNFD VDQNGNWLLQ GWKGRIVYAS
 SLWVPSSS*

Fig. 28AH

09265535-031099

```

----- LEUCINE HEPTAD I -----
----- A ----- B -----
SCL9 EVVLDRLSLIHCAQAVAADDRRCAGQLLKQIRLHSTPF-GDGNQRLAHCFANGLEARLAGTGSQIYKGT/SKP----PSAAPW/LPA
SCL14 ETADLRITLLVLCQAVSVDDRRTANVLRQIREHSSPL-GNGSERLAHYFANSLEARLAGTGTQIYTALSSKK----TSAADMLKA
SCL1 LSMVNELRQIVSIQ-GDPSQRLAAYMVEGLAARMAASGKFTYRALKCKE----PPSDEPLAA
SCL8 TSVCSRQTVMEIATALAEGKTEIATEILARVSQTPNLE-RNSEEKLVDPMVAALRSRIASPVTELY----GKE-----HLIS
SCL4 FDLEPPILLKAIYDCARISDSDPNEASKTLLQIRESVSELGDPTERVAFYFTEALSNNLSPNSPA-----TSSSSSSTEDLILS
SCL6 GPVGITEQLVKAAE-VTESDTCLAQGILARLNQQLSSPVGKPLERAAFYFKEALNNLLHNVSQT-----LNPYSLIFKIAA
SCL15 GGFGFIEDLIRVVDVCEDELQLAQVVLRLNQRLRSPAGRPLQRAAFYFKEALGSFLTGSNNRN-----PIRLSSWSEIVQIRIA
SCL18 AQNLLSILSLNSSPHGDSTERLVHLFTKALSVRINRQQQDQTAETVATWITNEMTMSNSTVFTSSVCKEQFLRTKNNSDFESCY
GAI NGVRLVHALLACAEAVQKENLTVAEALVKQIGFLAVSQIG-AMRQVATYFAEALARRIYRLSPS-----QSPIDHCLSDTL
RGA NGVRLVHALMACAEAIQQNNLTAEALVKQIGCLAVSQAG-AMRKVATYFAEALARRIYRLSPP-----QNQIHLSDTL
RGAL TGVRLVHALLACAEAVQQNNLKLADALVKHVGLLASSQAG-AMRKVATYFAEGLARRIYRIYPR-----DDVASSSFSDTL
SCR EGLHLLTLLQLCAEAVSADNLEEFANKLLLEISQ-LSTPYGTSARQVAAVFSEAMSARLLNSCLGIYAALPSRW-MPQTHSLKMVSA

```

```

----- VHIIID -----
AMEGEKM-----VHVIDLDASEPAQWLALLQAFNSRPEG-----PPLRLITGVVHQ-----
SCL3 HQFLACCPFRKLSYF ITNKTIRDLVGNLSQR-----VHVIDFGILYGFQWPTLIHRSFMYG-----SPKVRITGIEFPQGRFR
SCL9 YQTYMSVCPFKKAAIIFANHSMMRFTANANT-----IHIIDFGISYGFQWPAIHLRLSLRPGG-----SPKLRITGIELPQGRFR
SCL14 LAEFVDLTPWHRFGFIAANAAILDAVEGYSS-----VHVIDLSLTHCMQIPTLIDSMANKLHKKP-----PPLLRLTVIASDAEFHP
SCL16 ANVEILEAIAGETR-----VHIIDFQIAQGSQYMFILQELAKRPGG-----PPLLRLTVGVDDSQSRYA
SCL13 MHILYEACPYFKFGYESANGAIAEAVKNESF-----VHIIDFQISQGGQWVSLIRALGARPGG-----PPNVRITGIDDPSSFA
SCL5 MQVLFVPCPCFKFGFLAANGAILEAIKGESE-----VHIIDFIDQGNQYMTLIRSIAPLPGK-----RPRLRLTGIDDPESVQR
SCL1 TQLLYELSPCFKLGFEEANLAAILDAADNNDGMMIPHVIDFDIGEGGQVNNLRLTLSTRNKGKSQSQNSPVVKITAVANNVYGC
SCL8 YKTLNDACPYSKFAHLTANQAILEATEKSNK-----IHIIDFVDFGIVQGIQWPAIQLALATRTSGK-----PTQIRVSGIPAPSLG--
SCL4 YKSFSEISPVLFQFANFTSNQALLESFHFGR-----LHIIDFDIGYGGQWASLMQELVLRDNAA-----PLSLKITVFASPA
SCL6 IKEYSGISPIPLFSHTANQAILDSLSQSSSPF-VHVVDVEIFGFGGQYASLMREITEKSVS-----GGFLRVTAVA-----
SCL15 YLWLNQLTPFIRFGHLTANQAILDATETNDNGA--LHILDLDISQGLQWPLMQALAEARSSNPSSP--PPSLRITGICGRDVTGL-
SCL18 QMHFYETCPYLKFAHTANQAILEAFQGGKR-----VHVVDVSMQGLQWPAIQLALALRPGG-----PPVFRITGIGPPA----
GAI QMHFYETCPYLKFAHTANQAILEAFEGKKR-----VHVVDVSMQGLQWPAIQLALALREGG-----PPTFRITGIGPPA----
RGA QMHFYETCPYLKFAHTANQAILEAFEGKKR-----VHVVDVSMQGLQWPAIQLALALRPGG-----PPTFRITGIGPPA----
RGAL QMHFYETCPYLKFAHTANQAILEAFEGKKR-----VHVVDVSMQGLQWPAIQLALALRPGG-----PPTFRITGIGPPA----
SCR PQVFNGISPLVKFSHTANQAILEAFEGKEDS-----VHIIDLDIMQGLQWPAIQLALALRPGG-----PPHVRITGLGTSM-----

```

```

----- LEUCINE HEPTAD II -----
----- A ----- B -----
SCL3 -----EVLEQMAHRLIEEAEKLDIPFQFNPVVSRLDCLNVEQLRVK---TGEALAV @ DSFLNI
SCL11 KWKE-TITLDELMINPGETTVVNCIHLRQYTPDETIVSLDSPRDTVLKL
SCL9 ----PAQRVEETGQR-LAAYAKL-FGVPFYKAIKAWDA---IQLEDLDIDRDEITVVNCLYRAENLHDESVKVESCRDTVLNL
SCL14 ----PAEEFRQVIA-WLDTVSDTM--FRL-STTQLLRNGE-TIQVEDLKLROGEYVVVNSLFRFRNLDETIVLVNSPRDAVLKL
SCL16 PPLLGISYEELGSKLVNFATTRNVAMEFRIISSYSOGLSSLEQLRIDPFVFNEALVVNCHMMLHYIPDEILTSN-LRSVFLKE
SCL13 R---GGG---LSLVGERLATLAQSCGVPPFEHDAI-MSGCK--VQREHLGLEPGFAVVVNFPPVVLHMPDESVSVEKYRDRLLHL
SCL5 R---QGG---LELVGQRLGKLAEMCGVPFEFHGA-LCCTE--VEIEKLGVRNGEALAVNFPVLVHMPDESVTVENHRDRLRL
SCL1 S---IGG---LRIIGLRLEQLAEDNGVSFKFKAMP-SKTSI--VSPSTLGCKPGETLTIVNFAFQLHMPDESVTTVNQDELLHM
SCL8 VD--DGGEERLKAVGDLDSQLGDRIGISVSFNVVTSRLGD--LNRESLGCDDPDETAVNLAFKLYRVPDESVCCTENPRDELLRR
SCL4 ----ESPEPSLIATGNRLRDFAKVLDLNFDFIPILTPIHL---LNGSSFRVDPDEVLAVNFMQLYLKLLDET---PTIVDTAL-R
SCL6 ----NHQLELGFTQDNLKHFASEINISLDIQVLSLDLGSISWPNSS----EKEAVAVNISAA---S----FSLPLVLRFVKH
SCL15 ----EECAVETRLVKENLTQFAAEMKIRFQIEFVLMKTFEMLSFKAIR--FVEGERTVVLISPA---I----FRRLSGITDFVNN
SCL18 ----NRTGDRLTFRFADSLGQFQFHTLVITVEEDLAGLLQ---IRLLALSAVQGETTAVNCVHFLHKL----FNDDGDMIGHFL-
GAI ----PDNFDYLHEVGCKLAHLAEATHVEFEYRGFVANTLADLDASMLELRPSEIESVAVNSVFELHKL----LGRPGAIDKVLGV
RGA ----PDNSDHLHEVGCKLAQLAEATHVEFEYRGFVANSLADLDASMLELRPSEIESVAVNSVFELHKL----LGRPGGIEKVLGV
RGAL ----GYSILTDIQEVGWKLGQLASTIGVNFEFKSIANLNSDLKPEMLDIRPGLE-SVAVNSVFELHKL----LAHPGSIDKFLST
SCL19 ----EA----LQATGKRLSDFTDKLGLPFEFCPLAEKVGNDLT---ERLNVRKREAVAVH--WLQHSI----YDVTGSDAHTLWL
SCR

```

Fig. 29A

```

----- PFYRE -----
SCL3      -WGLSPKVMVTEQDS---DHNGSTLMERLLESLYTYAALFDCLTKVPTSQDRIKA-VEKMLFGEEIKXNI-----SCEGFER
SCL11     FRDINPDLFVFAEING---MYNSPFTMTFRFREALFHYSSLFDMFDTTHAEDEVKNFSLLERELLVRDAMSVI-----SCEGAER
SCL9      IGKINPDLFVFGIVNG---AYNAPFVTRFRFREALFHFSSIFDMLETIVPREDEERMF--LEMEVFGREALNVI-----ACEGWER
SCL14     IRKINPNVFIPIAILSG---NYNAPFVTRFRFREALFHYSAVFDMDCKSLAREDEMRLM--YVEFYGREIVNVV-----ASEGTER
SCL16     LRDLNPTIVTILIDEDSDFTSTN                                     NVV-----AKEGAER
SCL13     IKSLSPKLVTLVEQES---NINTSPLVSRFVETLDYYTAMFESIDAARPRDDKQRIIS--AEQHCVARDIVNMI-----ACESEER
SCL5      VKHLSPNVVTLEVEQA---NINTAPFLPRFVETMNHYLAVFESIDVKLARDHKERIN--VEQHCLAREVVNLI-----ACEGVER
SCL1      VKSLNPCLVTVVEQDV---NINTSPFFPRFIEAYEYYSVAVFESLDMTLPRESQERMN--VERQCLARDIVNIV-----ACEGEER
SCL8      VKGLKPRVVTLEVEQEM---NSNTAPFLGRVSESCACYGALLESVESTVPSTNSERAK--VEEG-IGRKLVNAV-----ACEGIDR
SCL4      LAKLNPRVVTLEGEYEV---SLNRVGFANRVKNAQFYSAVFESLEPNLGRDSEERV--VERELFGRISGLIGPEK---TGIHR
SCL7      L-----SPTIIVCSDRGC---ERTDLPFSQQLAHSLSHTALFESLDA-VNANLDAMQK--TERFLIQPEIEKLV-----LDR
SCL6      LRRVSPKVVVFDSEGWTEIAGSGSFRREFVSALEFYTMVLESLDAAAPPGDLVKKI--VEAFVLRPKISAAB-----ETAA-DR
SCL15     -SAIKSLNSRIVTMAEREANGHDHSHFLNRFSEAVDHYMAIFDSLEATLPPNSRERLT--LEQRWFQKEILDVV--AAEETERKQR
SCL18     VNQIKPEIFTVVEQES---NHNSPIFLDRFTESLHYSTLFDLSLEGV--PSQDKVM--SEVYL-GKQICNVV-----ACDGPDR
GAI       VKQIKPVIFTVVEQES---NHNGPVFLDRFTESLHYSTLFDLSLEGV--PNSQDKVM--SEVYL-GKQICNLV-----ACEGPD
RGA       IKSIRPDIMTVVEQEA---NHNGTVFLDRFTESLHYSSLFDSLEGP--PSQDRVM--SELFL-GRQILNLV-----ACEGEDR
RGAL      VKAIKPSIVTVVEQEA---NHNGIVFLDRFNEALHYSSLFDSLEDSYSLPSQDRVM--SEVYL-GRQILNVV-----AAEGSDR
SCL19     LQRLAPKVTVVEQD---LSHAGSFLGRFVEATHYYSALFDSLGSYGEESEERHV--VEQQLLSKEIRNVL-----AVGGPSR
SCR

```

```

----- SAW -----
SCL3      RERHEK-LEKWSQRIDLAGFGNVPLSYYAMLQARRLLQG-CGFDGYR-IKEESGCAVICWQDRPLYSVSAWRCRK
SCL11     FARPET-YKQWRVRIIRAGFKPATISKQIMKEAKEIVRK-RYHRDFVI-DSDNNWMLQGKGRVITYAFSCWKPAEKFTNNNLNI
SCL9      VERPET-YKQWHVVRAMRSGLVQVPFDPISIMKTSLHKVHT-FYHKDFVI-DQDNRWLLQGKGRVIMALSVMKPS
SCL14     VESRET-YKQWQARLIRAGFRQLPLEKELMQLKLIEN-GYDKNFIV-DQNGNWLQGWKGRVITYASSLWVPSSS
SCL16     VERLEP          FTGVGFGETAMTEVKTMLEEATGWGMKKDVEDDNDVERFVLTKWGHVSMFASAWAPPN
SCL13     VERHEV-LGKWRVRMMAGFTGWVSTSAFAASEMLKA--YDKNYKL-GGHEGALYLFWKRRPMATCSVWKPNPNYIG
SCL5      EERHEP-LGKWRSRFHMAGFKPYPLSSYVNATIKGLLES--YSEKYTL-EERDGLYLGWKNQPLITSCAWR
SCL1      IERYEA-AGKWRARMMAGFNPKPMSAKVTNNIQNLIKQ-QYCNKYKL-KEEMGELHFCWEKSLIVASAWR
SCL8      IERCEV-FGKWRMRMSMAGFELMPLSEKIAESMKSR-GN-RVHPGFTV-KEDNGGVCFGWMGRALTIVASAWR
SCL4      ERMEE--KEQWRVLMENAGFESVKLSNYAVSQAKILLWNYNYSNLYSIVESKPGFISLAWNDLPLLTSSWR
SCL7      FGLMEE-KEQWRVLMENAGFEPKPSNYAVSQAKILLWNYNYSNLYSIVESKPGFISLAWNNVPLLTSSWR
SCL6      SRPIERPMTWQAMFLQMGFSPVTHSNFTESQAECLVQR-TPVRGFH-VEKHNLSLLLCWQRTLVGVSAWRCRSS
SCL15     RHTGE---MTWREAFCAAGMRPIQQSQFADFQAECLLEK-AQVRGFH-VAKRQELVLCWHGRALVATSAWR
SCL18     HRRFE---IWEEMMKRFGFVNVPIGSFALSQAKLLRL-HYSEGYN-LQFLNNSLFLGWQNRPLFSVSSW
GAI       VERHET-LSQWRNRFGSAGFAAAHIGSNAFKQASMLLALFNGGEGYR-VEESDGCLMLGWHTRPLIATSARKLSTN
RGA       VERHET-LSQWGNRFGSSGLAPAHLSNAFKQASMLLSVFNSGQGYR-VEESNGCLMLGWHTRPLITTSARKLSTAA
RGAL      VERHET-LNQWRNRFGGLGFKPVSIGSNAYKQASMLLALYAGADGYN-VEENEGCLMLGWHTRPLIATSARKLRNVE
SCL19     VERHET-AAQWRIRMKSAFDPHILGSSAFKQASMLLSLYATGDGYR-VEENDGCLMIRWQTRPLITTSARKLA
SCR      --SGEVKFEWREKMQCGFKGISLAGNAATQATLLGMFP--SDGYTLVDDN-GTLKLGWKDLSLLTASAWTPRS

```

@SSVLQLHTFLASDDDLMRKNCALRFHNNPSGVDLQVRVLMMSHGSAEARENDMSNNGYSPSGDSASSLPLPSSGRT

Fig. 29B

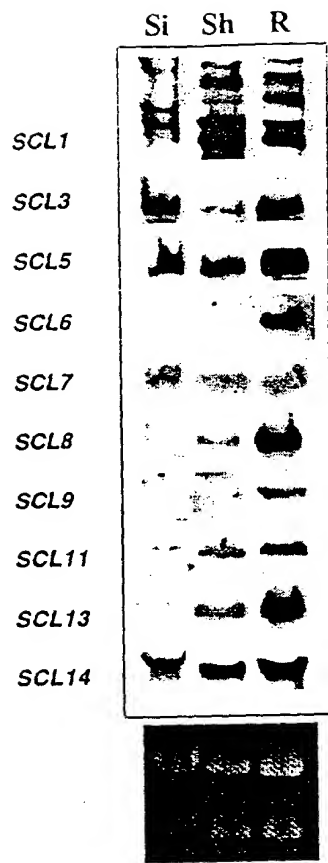


Fig. 30

09265585 .031099

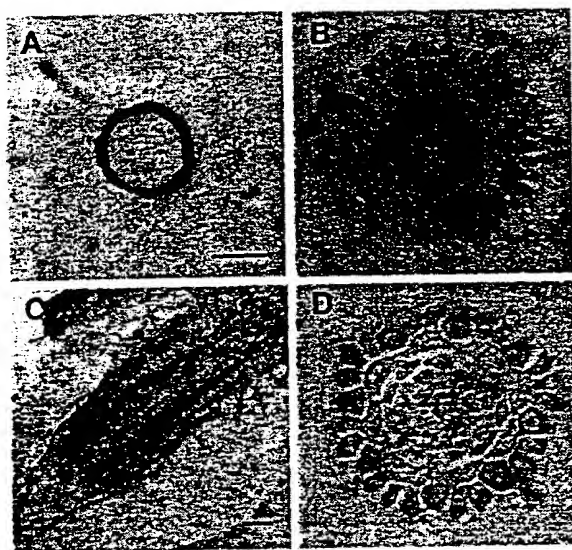
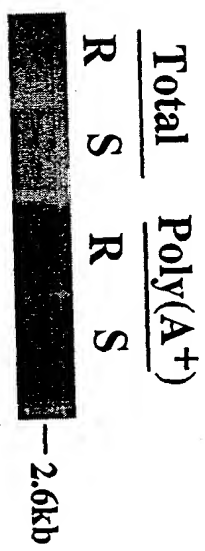


Fig. 31

RNA Blot Analysis



Either total RNA or poly (A⁺) RNA was probed with the full length of cDNA.
 About 2.6kb fragment was hybridized to the probe.
 R: Roots, S: Shoots

CBPBT44 partial cDNA sequence

GCGGCCGCGCAGAGCCGCGCGTGGCGGTGGCGTTCCAGGCGTACAACGCGCTGTCGCCG
CTCGTCAAGTTCTCGCACTTCACGGCCAACCAGGCCATCCTGCAGGCGCTCGACGGCGAG
GACTGCCTCCACGTGATCGACCTGGACATCATGCAGGGCCTGCAGTGGCCGGGGCTCTTC
CACATCCTCGCGTCCCGCCCGCGCAAGCCGCGGTGCTCCGGATCACCGGGCTCGGCGCG
TCGCTCGACGTCCTCGAGGCCACTGGCCGCGCCTCGCCGACTTCGCGGCCTCGCTCGGC
CTCCCGTTTCGAGTTCCGCCCCATCGAGGGGAAGATCGGGCACGTGCGCCGACGCCGCGGCG
CTCCTCGGCTCGCGCCAGCGGCGGGGATGACGAGGCCACCGTGGTGCACCTGGATGCAC
CACTGCCTCTATGACGTGACGGGGTCGGACGTGGGCACGGTGCGGCTGCTCCGGAGCCTG
CGCCGAAGCTGATCACCATCGTGGAGCAGGACCTGGGCCACAGCGGCGATTTCCTGGGC
CGGTTTCGTGGAGGCGCTGCACTACTACTCGGCGCTGTTTCGACGCGCTGGGAGACGGCGCC
GGCGCGGCCGAGGAGGAGTCGGCCGAGCGGTACGCGGTTGAGCGACAGCTCCTGGGCGCG
GAGATACGCAACATCGTGGCCGTAGGGGGGCCCAAGCGGACAGGGGAGGTGCGCGTGGAG
CGGTGGAGCCACGAACCTGCGGCACGCCGGGTTCCGGCCAGTGTCCCTGGCCGGGAGCCCT
GCCGCGCAGGCCAGGCTGCTCCTCGGCATGTATCCGTGGAAGGGGTACACGCTGGTGGAG
GAGGACGCGTGCTTAAGCTGGGCTGGAAGGACCTCTCCCTGCTCACCGCGTCGGCGTGG
GAGCCGGCGGACGACGCTGCCGCTTCTGCGCCACCGGTTAACGAGTACGAGCGGACGCG
TGGGTCGAC

CBPBT44 partial amino acid sequence

AAQSRRVAVAFQAYNALSPVKFSHFTANQAILQALDGEDCLHVIDLDIMQGLQWPGLF
HILASRPKRPSLRITGLGASLDVLEATGRRRLADFAASLGLPFEFRPIEGKIGHVADAAA
LLGSRRRRDDEATVVHWMHCLYDVTGSDVGTVRLRLRSLRPKLITIVEQDLGHSGLDFG
RFVEALHYYSALFDALGDGAGAAEEESAERYAVERQLLGAIEIRNIVAVGGPKRTGEVRVE
RWSHEL RHAGFRPVSLAGSPAAQARLLLGMPWKGYTLVEEDACLKLGWKDLSLLTASAW
EPADDAAASAPTGXRVRAAWVD

Fig. 33

09065585-031099

Zm SCR
CBPBT44
At SCR

GRVAAAFQVF NGISPFVKFS
RRVAVAFQAY NALSPLVKFS
LKMVSAFQVF NGISPLVKFS

Zm SCR HFTANQAIQE AFEREERVHI IDLDIMQGLQ WPGLFHILAS RPGGPPRVRL
CBPBT44 HFTANQAILQ ALDGEDCLHV IDLDIMQGLQ WPGLFHILAS RPRKPRSLRI
At SCR HFTANQAIQE AFEKEDSVHI IDLDIMQGLQ WPGLFHILAS RPGGPPHVRL

Zm SCR TGLGASMEAL EATGKRLSDF ADTLGLPFEF CAVA EKAGNV DPEKLGVTTR
CBPBT44 TGLGASLDVL EATGRRLLADF AASLGLPFEF RPIEGKIGHV ADAAALLGSR
At SCR TGLGTSMEAL QATGKRLSDF TDKLGLPFEF CPLAEKVGNL DTERLNVKR

Zm SCR -----EAVA VHWHHSLYD VTGSDSNTLW LIQRLAPKVV TMVEQDLSHS
CBPBT44 QRRRDDEATV VHWMHCLYD VTGSDVGTVR LLRSLRPKLI TIVEQDLGHS
At SCR -----EAVA VHWLQHSYD VTGSDAHTLW LLQRLAPKVV TVVEQDLSHA

Zm SCR GSFLARFVEA IHYYSALFDS LDASYGEDSP ERHV---VEQ QLLSREIRNV
CBPBT44 GDFLGRFVEA LHYYSALFDA LGDGAGAAEE ESAERYAVER QLLGAEIRNI
At SCR GSFLGRFVEA IHYYSALFDS LGASYGEESE ERHV---VEQ QLLSKEIRNV

Zm SCR LAVGGPARTG DVKFGSWREK LAQSGFRAAS LAGSAAAQAS LLLGMFSPDG
CBPBT44 VAVGGPKRTG EVRVERWSHE LRHAGFRPVS LAGSPAAQAR LLLGMPWPKG
At SCR LAVGGPSRSG EVKFESWREK MQQCGFKGIS LAGNAATQAT LLLGMFSPDG

Zm SCR YTLVEENGAL KLGWKDLCLL TASAWRPIQV PPCR
CBPBT44 YTLVEEDACL KLGWKDLSLL TASAWEPADD AAASAPTG
At SCR YTLVDDNGTL KLGWKDLSLL TASAWTPRS

09265585-031099

Fig. 34

DNA Blot Analysis

